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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:09:54 ; Search time 225.955 Seconds
(without alignments)
349.180 Million cell updates/sec

Title: US-10-828-343-2
Perfect score: 1095
Sequence: 1 MCWFKLWSLLVGSLLVSGT.....GQAVRVLDSIPDVPDVK 204

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	204	2 AAW40103	Aaw40103 Human her
2	1095	100.0	204	2 AAW23944	Aaw23944 Human her
3	1095	100.0	204	2 AAW74570	Aaw74570 Kaposi sa
4	992	90.6	185	2 AAW95015	Aaw95015 Kaposi's
5	188	17.2	184	2 AAW02611	Aaw02611 Interleuk
6	187	17.1	184	2 AAW02610	Aaw02610 Interleuk
7	186	17.0	183	8 ADL89593	Adl89593 Human mod
8	185.5	16.9	184	2 AAW08477	Aaw08477 Interleuk
9	185.5	16.9	570	6 ABP72702	Abp72702 Human int
10	184.5	16.8	184	2 AAW08476	Aaw08476 Interleuk
11	184	16.8	183	8 ADL89567	Adl89567 Human mod
12	184	16.8	201	1 AAP81162	Aap81162 Polypepti
13	184	16.8	212	5 AAU99248	Aau99248 Human int
14	184	16.8	212	5 AAU99249	Aau99249 Human int
15	184	16.8	212	5 AAU99250	Aau99250 Human int
16	184	16.8	212	5 AAU99601	Aau99601 Human int
17	183.5	16.8	184	2 AAW07200	Aaw07200 Human int
18	183.5	16.8	184	2 AAW58519	Aaw58519 Human int
19	183.5	16.8	184	2 AAW32803	Aaw32803 Human IL-
20	183.5	16.8	500	2 AAW36847	Aaw36847 Human fus
21	183.5	16.8	525	2 AAW36846	Aaw36846 Human fus
22	183	16.7	169	2 AAR77387	Aar77387 Human IL-
23	183	16.7	183	8 ADL89594	Adl89594 Human mod
24	183	16.7	183	8 ADL89586	Adl89586 Human mod
25	183	16.7	183	8 ADL89584	Adl89584 Human mod

26	183	16.7	183	8 ADL89566	Adl89566 Human mod
27	183	16.7	185	2 AAR45718	Aar45718 Full leng
28	183	16.7	185	2 AAR45720	Aar45720 Full leng
29	183	16.7	211	2 AAR25279	Aar25279 Mutant hu
30	183	16.7	212	1 AAP70238	Aap70238 Interfero
31	183	16.7	212	1 AAP80269	Aap80269 Recombina
32	183	16.7	212	1 AAP90469	Aap90469 Interleuk
33	183	16.7	212	1 AAP90436	Aap90436 Interfero
34	183	16.7	212	1 AAP90047	Aap90047 pBSF2-L8
35	183	16.7	212	1 AAP90371	Aap90371 pBSF2-L8
36	183	16.7	212	2 AAR05415	Aar05415 Human B-c
37	183	16.7	212	2 AAR33430	Aar33430 IFN-beta-
38	183	16.7	212	2 AAR34726	Aar34726 Human IL-
39	183	16.7	212	2 AAR49249	Aar49249 Sequence
40	183	16.7	212	2 AAR49041	Aar49041 Human int
41	183	16.7	212	2 AAR72317	Aar72317 Interfero
42	183	16.7	212	2 AAW33643	Aaw33643 Human int
43	183	16.7	212	2 AAW35878	Aaw35878 Human int
44	183	16.7	212	3 AAY87816	Aay87816 Human IL-
45	183	16.7	212	5 AAE15825	Aae15825 Human int

ALIGNMENTS

RESULT 1
AAW40103
ID AAW40103 standard; protein; 204 AA.
XX AC AAW40103;
XX DT 27-AUG-2003 (revised)
DT 15-JUL-1998 (first entry)
XX DE Human herpesvirus 8 (HHV-8) interleukin-6.
XX DL-B; thymidylate synthase; dihydrofolate reductase; primer; HHV-8;
KW Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein;
KW Kaposi's sarcoma; beta-chemokine-like; amplification; PCR; VIL-6.
XX OS Human herpesvirus 8.
XX PN WO9804284-A1.
XX PD 05-FEB-1998.
XX PF 24-JUL-1997; 97WO-US012931.
XX PR 25-JUL-1996; 96US-0022591P.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Hayward GS, Nicholas J, Reitz MR, Hardwick JM;
XX WPI; 1998-130422/12.
XX New human herpes virus gene region containing 8 open reading frames -
XX useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based large
XX cell lymphoma.
XX Claim 1; Page 59-60; 84pp; English.
XX The sequence represents a novel human herpesvirus 8 (HHV-8) interleukin-
XX 6. The invention claims for novel genes, which includes the viral
XX interleukin-6 gene, found at the divergent DL-B locus. HHV-8 divergent
XX locus DL-B lies between open reading frames 11 and 17. Sequencing of the
XX HHV-8 divergent locus DL-B revealed the presence of nine viral ORFs with
XX gene products related to cellular proteins. These proteins include the
XX thymidylate synthase (TS, AAW40100), dihydrofolate reductase (DHFR, see
XX AAW40101), Bcl-2 homologue (AAW40102), IE-1A (AAW40107), IE-1B (AAW40108)
XX and, four cytokines which include viral interleukin-6 (VIL-6), viral
XX macrophage inhibitory protein (vMIP)-1A (AAW40104) and -1B (AAW40105) and
XX beta-chemokine-like (BCK, AAW40106) protein. The invention claims the

CC mentioned proteins and a polynucleotide containing HHV-8 genes encoding
 CC one or more of these proteins. The invention also claims that the
 CC polynucleotide and the proteins may be used directly or indirectly, e.g.
 CC using antibodies to the proteins, to diagnose an HHV-8 associated
 CC disease, e.g. Kaposi's sarcoma, Castlemann's disease, multiple myeloma and
 CC body cavity based large cell lymphoma (BCBL). The proteins have also been
 CC claimed to be useful in screening compounds for drugs to treat HHV-8
 CC diseases. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 204 AA;

Query Match 100.0%; Score 1095; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.2e-117;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCWFKLSLLVSGSLVSGTRGKLPDAPFEKDLIIQRLNMLWVIDECFRDLCYRTGIC 60
 DB 1 MCWFKLSLLVSGSLVSGTRGKLPDAPFEKDLIIQRLNMLWVIDECFRDLCYRTGIC 60
 QY 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKADGFEFEVLPKFLTTTFGKSVI 120
 DB 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKADGFEFEVLPKFLTTTFGKSVI 120
 QY 121 NVDVMELLTKLGDWIOBELNKLTKTHYSPKFDRLGLRQLGKLYWVRHFPASFYVLSAM 180
 DB 121 NVDVMELLTKLGDWIOBELNKLTKTHYSPKFDRLGLRQLGKLYWVRHFPASFYVLSAM 180
 QY 181 EKFAQAVRVLDSPDVTDPVHDK 204
 DB 181 EKFAQAVRVLDSPDVTDPVHDK 204

RESULT 2
 AAW23944
 ID AAW23944 standard; protein; 204 AA.

XX AC AAW23944;
 XX 30-JUN-1998 (first entry)
 XX Human herpesvirus 8 interleukin-6.
 DE interleukin-6; IL-6; human herpesvirus 8; HHV8; shotgun-cloning;
 KW antibody; diagnosis; treatment.
 XX Human herpesvirus 8.
 XX WO9803657-A1.
 PN 29-JAN-1998.
 PD 19-JUL-1996; 96WO-EP003199.
 PF 19-JUL-1996; 96WO-EP003199.
 PR (BEHW) BEHRING DIAGNOSTICS GMBH.
 PA (UYN) UNIV NEW YORK STATE.
 XX Fleckenstein B, Albrecht J, Neipel F, Friedman-Kien A, Huang Y;
 WPI; 1998-120781/11.

XX Viral interleukin-6 produced recombinantly from human herpes virus 8 DNA
 PT - and related nucleic acid and antibodies, used for diagnosis and
 PT treatment of herpes 8 infection or related diseases, e.g. Kaposi sarcoma.
 XX Claim 2; Fig 2; 19pp; English.

XX The interleukin-6 (IL-6) and protein AAW23945 derived from the sequence
 CC can be used to detect antibodies and antibodies can be used to detect IL-
 CC 6. This can be used for the diagnosis of HHV8 infection or associated
 CC diseases such as Kaposi sarcoma or kidney cell carcinoma. Antibodies,
 CC proteins and the gene sequence can all be used in the treatment of

CC infections and diseases as mentioned above
 XX
 SQ Sequence 204 AA;
 Query Match 100.0%; Score 1095; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.2e-117;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCWFKLSLLVSGSLVSGTRGKLPDAPFEKDLIIQRLNMLWVIDECFRDLCYRTGIC 60
 DB 1 MCWFKLSLLVSGSLVSGTRGKLPDAPFEKDLIIQRLNMLWVIDECFRDLCYRTGIC 60
 QY 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKADGFEFEVLPKFLTTTFGKSVI 120
 DB 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKADGFEFEVLPKFLTTTFGKSVI 120
 QY 121 NVDVMELLTKLGDWIOBELNKLTKTHYSPKFDRLGLRQLGKLYWVRHFPASFYVLSAM 180
 DB 121 NVDVMELLTKLGDWIOBELNKLTKTHYSPKFDRLGLRQLGKLYWVRHFPASFYVLSAM 180
 QY 181 EKFAQAVRVLDSPDVTDPVHDK 204
 DB 181 EKFAQAVRVLDSPDVTDPVHDK 204

RESULT 3
 AAW74570
 ID AAW74570 standard; protein; 204 AA.
 XX AC AAW74570;
 XX 04-DEC-1998 (first entry)
 XX Kaposi sarcoma herpes-like virus/interleukin-6.

XX Kaposi sarcoma herpes-like virus/interleukin-6; PCR; primer;
 KW antiviral agent; multiple myeloma; vaccine; rheumatoid arthritis;
 KW monoclonal gammopathy of undetermined significance; MGUS; malignant;
 KW interleukin-6; Alzheimer's disease; multiple sclerosis; scleroderma;
 KW systemic lupus erythematosus; amplification.
 XX Synthetic.
 XX WO9835684-A2.
 XX 20-AUG-1998.
 XX 12-FEB-1998; 98WO-US002820.
 XX 14-FEB-1997; 97US-00800710.
 XX 11-NOV-1997; 97US-00967504.
 XX (BERE/) BERENSON J R.
 XX (RETT/) RETTIG M B.
 XX (VESC/) VESCIO R A.
 XX Berenson JR, Rettig MB, Vescio RA;
 WPI; 1998-480765/41.
 XX N-PSDB; AAV54070.

XX Treatment of multiple myeloma and monoclonal myopathy with antiviral
 PT agent - active against Kaposi sarcoma virus, or with inhibitory nucleic
 PT acid or antibody against this virus.
 XX Disclosure; Fig 5B; 137pp; English.
 XX This is the amino acid sequence of the kaposi sarcoma herpes-like
 CC virus/interleukin-6, used in the method of the invention. In this method,
 CC an antiviral agent effective against Kaposi sarcoma herpes-like virus
 CC (KSHV), is used to prevent progression of MGUS to multiple myeloma or
 CC related malignancy. KHSV- and/or interleukin-6 related disorders such as
 CC specifically Alzheimer's disease, multiple sclerosis, rheumatoid

CC arthritis, systemic lupus erythematosus, scleroderma and malignancies of
CC kidney or head/neck. The vaccines (comprising a KHSV-specific immunogen)
CC is used to produce a therapeutic and/or prophylactic response
XX
SQ Sequence 204 AA;

Query Match 100.0%; Score 1095; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.2e-117;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCFKLSLLVSGSLVSGTRGKLPDAPPEKDLIIQRLNMLWVIDECFRLCYRTGIC 60
Db 1 MCFKLSLLVSGSLVSGTRGKLPDAPPEKDLIIQRLNMLWVIDECFRLCYRTGIC 60

Qy 61 KGILEPAAIFHLKLPAINDDHCLGIGNFNETSCLKKLADGFFFEVLFKELTTFEGKSVI 120
Db 61 KGILEPAAIFHLKLPAINDDHCLGIGNFNETSCLKKLADGFFFEVLFKELTTFEGKSVI 120

Qy 121 NVDVWELLTKLWDIOEELNKLTKTHYSPPKFDRGLLQGLKYVWRHFASFYVLSAM 180
Db 121 NVDVWELLTKLWDIOEELNKLTKTHYSPPKFDRGLLQGLKYVWRHFASFYVLSAM 180

Qy 181 EKFAQAVRVLDSIPDVTDPVHDK 204
Db 181 EKFAQAVRVLDSIPDVTDPVHDK 204

RESULT 4
AAW95015
ID AAW95015 standard; peptide; 185 AA.
XX AAW95015;
AC
XX
XX 27-AUG-2003 (revised)
DT 21-MAY-1999 (first entry)
XX
XX Kaposi's sarcoma herpes virus interleukin-6 (IL-6) polypeptide.
BE
XX Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;
KW inflammatory condition; drug screening; human; IL-6.
XX
XX Human herpesvirus 8.
OS
XX WO9905280-A1.
PN
XX
XX
XX
XX 04-FEB-1999.
PD
XX
XX 24-JUL-1998; 98WO-US015423.
PF
XX
XX 25-JUL-1997; 97US-00900905.
PR
XX
XX (SCHE) SCHERING CORP.
PA
XX
XX Bajan JP;
PI
XX
XX WPI; 1999-142935/12.
DR
XX
XX Newly isolated or recombinant polynucleotide encoding mammalian cytokine
PT interleukin-B30 (IL-B30), including fragments - useful for regulating
PT activation, development, differentiation and function of various cell
PT types, and for diagnosing and treating conditions associated with IL-B30.
XX
XX Disclosure; Page 11-12; 83pp; English.
PS
XX
XX This invention relates to mammalian cytokine interleukin-B30 (IL-B30)
CC polypeptides. Host cells containing a vector comprising the IL-B30
CC nucleic acids are used for the recombinant production of the proteins.
CC The polynucleotides are useful for diagnosis of IL-B30 mediated
CC conditions, and forensic science (e.g. to distinguish rodent from human,
CC or as a marker to distinguish between different cells exhibiting
CC differential expression or modification patterns). The IL-B30 (including
CC fragments), together with antibodies that bind to IL-B30 are useful for
CC teaching purposes. They are also used for treating conditions associated

CC with abnormal physiology or development, including inflammatory
CC conditions. The polypeptide cytokine should mediate cytokine synthesis
CC and proliferation in cells. IL-B30 is useful for drug screening to
CC identify compounds having binding affinity to IL-B30. The present
CC -AUG-2003 to correct OS field.)
XX
SQ Sequence 185 AA;

Query Match 90.6%; Score 992; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 8.2e-106;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 TRGKLPDAPPEFEDLLIQLNMLWVIDECFRLCYRTGICKGLEPAAIFHLKLPAIND 79
Db 1 TRGKLPDAPPEFEDLLIQLNMLWVIDECFRLCYRTGICKGLEPAAIFHLKLPAIND 60

Qy 80 TDHCGILGNETSCLKKLADGFFFEVLFKELTTFEGKSVINVDVWELLTKLWDIOEE 139
Db 61 TDHCGILGNETSCLKKLADGFFFEVLFKELTTFEGKSVINVDVWELLTKLWDIOEE 120

Qy 140 LNKLTTHYSPPKFDRGLLQGLKYVWRHFASFYVLSAMEKFAQAVRVLDSIPDVT 199
Db 121 LNKLTTHYSPPKFDRGLLQGLKYVWRHFASFYVLSAMEKFAQAVRVLDSIPDVT 180

Qy 200 DVHDK 204
Db 181 DVHDK 185

RESULT 5
AAW02611
ID AAW02611 standard; protein; 184 AA.
XX
AC AAW02611;
XX
XX 25-MAR-2003 (revised)
DT 24-FEB-1997 (first entry)
XX
XX Interleukin-6 (F74Y, Q75P, S76I, Q175I, S176R, Q183A).
DE
XX
XX Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist;
KW bovine; granulocyte colony stimulating factor; bc-CSF; receptor; gp130;
KW thrombocytopoiesis; haematopoietic progenitor cell; rheumatoid arthritis;
KW bone marrow transplantation; gene therapy; multiple myeloma; leukaemia;
KW breast cancer; infectious disease; bone marrow progenitor cell; therapy;
KW postmenopausal osteoporosis; systemic lupus erythematosus; hormone.
XX
XX Homo sapiens.
OS
XX
XX
XX Key Location/Qualifiers
PH
FT Misc-difference 74 /note= "F74Y"
FT Misc-difference 75 /note= "Q75P"
FT Misc-difference 76 /note= "S76I"
FT Misc-difference 175 /note= "Q175I"
FT Misc-difference 176 /note= "S176R"
FT Misc-difference 183 /note= "Q183A"
XX
XX WO9618648-A1.
PN
XX
XX 20-JUN-1996.
PD
XX
XX 13-DEC-1995; 95WO-IT000216.
PF
XX
XX 14-DEC-1994; 94IT-RM000805.
PR
XX
XX (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.

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XX
PI Ciliberto G, Savino R, Lahm A, Toniatti C;
DR WPI; 1996-300575/30.
XX
PT Identifying interleukin-6 super-agonists and (super)antagonists - using a
PT 3-dimensional model of bovine granulocyte colony stimulating factor to
PT identify binding sites.
XX
PS Claim 8; Page ?; 26pp; English.
XX
CC AAW02610-W02612 represent human interleukin-6 (IL-6) mutants (see
CC AAW02609 for wild type sequence), with an increased specificity for the
CC specific receptor. These sequences were identified using the method of
CC the invention. The method comprises comparing IL-6 with the sequence of
CC the bovine granulocyte colony stimulating factor (bG-CSF). On the basis
CC of this comparison a 3-dimensional model of IL-6 is formulated, which
CC allows the identification of residues that form the site of interaction
CC with the specific receptor, and those that constitute the site of
CC interaction with gp130. The method can be used to identify superagonists,
CC antagonists, and superantagonists of IL-6. The IL-6 superagonists
CC identified by this method can be used for the treatment of
CC thrombocytopaenia, and for the ex vivo expansion of human haematopoietic
CC progenitor cells for bone marrow transplantation and gene therapy. They
CC can also be used for the treatment of breast cancer, leukaemia, and
CC infectious diseases or diseases connected with disorders of bone marrow
CC progenitor cells. The antagonists and superantagonists identified by the
CC method (see AAW08476-W08478) can be used for the treatment of diseases
CC characterised by the overproduction of IL-6, particularly multiple
CC myeloma, rheumatoid arthritis, postmenopausal osteoporosis, and systemic
CC lupus erythematosus. The method can also be used to identify IL-6
CC variants with a greater affinity for the specific receptor, or variants
CC with a reduced or abolished affinity for gp130. (Updated on 25-MAR-2003
CC to correct PR field.)
XX
SQ Sequence 184 AA;
*Query Match 17.2%; Score 188; DB 2; Length 184;
Best Local Similarity 26.2%; Pred. No. 5.8e-13;
Matches 43; Conservative 38; Mismatches 83; Indels 0; Gaps 0;
QY 28 PEFKDLIIQRLNWMWVDECDFRDLVYRTGICKGILEPAAIFHLKLPAINDTDHCGLIG 87
DB 18 PLTSSERIDKQIRYILDGISALRKETCNKSNWCESSKEALAENNLNPKMAEKDCYFIG 77
QY 88 FNETSLCKKLADGPFEEVFLFKLTTEFGKSVINVDVNMELLTKTLGWDIQBELNKLTKTH 147
DB 78 FNEETCLVKIITGLLEFEVYLYLQNRPFESSEBQARAVQMTKVLQFLQKAKNLDAIT 137
QY 148 YSPPKFDRGLLQGLKLVVRFHAFSYVLSAMEKFAQAVRVL 191
DB 138 TPDPTNASLLTKLQANQWQMDTTHLIRSFKEFLIRSLAL 181
RESULT 6
AAW02610
ID AAW02610 standard; protein; 184 AA.
XX
AC AAW02610;
XX
DT 25-MAR-2003 (revised)
DT 24-FEB-1997 (first entry)
XX
DE Interleukin-6 (Q75Y, S76I, Q175I, S176R, Q183A).
XX
KW Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist;
KW bovine; granulocyte colony stimulating factor; bG-CSF; receptor; gp130;
KW thrombocytopaenia; haematopoietic progenitor cell; rheumatoid arthritis;
KW bone marrow transplantation; gene therapy; multiple myeloma; leukaemia;
KW breast cancer; infectious disease; bone marrow progenitor cell; therapy;
KW postmenopausal osteoporosis; systemic lupus erythematosus; hormone.
XX
OS Homo sapiens.

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XX
FH Key Location/Qualifiers
FT Misc-difference 75 /note= "Q75Y"
FT Misc-difference 76 /note= "S76I"
FT Misc-difference 175 /note= "Q175I"
FT Misc-difference 176 /note= "S176R"
FT Misc-difference 183 /note= "Q183A"
XX
PN W09618648-A1.
XX
PD 20-JUN-1996.
XX
PF 13-DEC-1995; 95WO-IT000216.
XX
PR 14-DEC-1994; 94IT-RM000805.
XX
PA (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
XX
PI Ciliberto G, Savino R, Lahm A, Toniatti C;
XX
DR WPI; 1996-300575/30.
XX
PT Identifying interleukin-6 super-agonists and (super)antagonists - using a
PT 3-dimensional model of bovine granulocyte colony stimulating factor to
PT identify binding sites.
XX
PS Claim 8; Page ?; 26pp; English.
XX
CC AAW02610-W02612 represent human interleukin-6 (IL-6) mutants (see
CC AAW02609 for wild type sequence), with an increased specificity for the
CC specific receptor. These sequences were identified using the method of
CC the invention. The method comprises comparing IL-6 with the sequence of
CC the bovine granulocyte colony stimulating factor (bG-CSF). On the basis
CC of this comparison a 3-dimensional model of IL-6 is formulated, which
CC allows the identification of residues that form the site of interaction
CC with the specific receptor, and those that constitute the site of
CC interaction with gp130. The method can be used to identify superagonists,
CC antagonists, and superantagonists of IL-6. The IL-6 superagonists
CC identified by this method can be used for the treatment of
CC thrombocytopaenia, and for the ex vivo expansion of human haematopoietic
CC progenitor cells for bone marrow transplantation and gene therapy. They
CC can also be used for the treatment of breast cancer, leukaemia, and
CC infectious diseases or diseases connected with disorders of bone marrow
CC progenitor cells. The antagonists and superantagonists identified by the
CC method (see AAW08476-W08478) can be used for the treatment of diseases
CC characterised by the overproduction of IL-6, particularly multiple
CC myeloma, rheumatoid arthritis, postmenopausal osteoporosis, and systemic
CC lupus erythematosus. The method can also be used to identify IL-6
CC variants with a greater affinity for the specific receptor, or variants
CC with a reduced or abolished affinity for gp130. (Updated on 25-MAR-2003
CC to correct PR field.)
XX
SQ Sequence 184 AA;
Query Match 17.1%; Score 187; DB 2; Length 184;
Best Local Similarity 26.2%; Pred. No. 7.5e-13;
Matches 43; Conservative 38; Mismatches 83; Indels 0; Gaps 0;
QY 28 PEFKDLIIQRLNWMWVDECDFRDLVYRTGICKGILEPAAIFHLKLPAINDTDHCGLIG 87
DB 18 PLTSSERIDKQIRYILDGISALRKETCNKSNWCESSKEALAENNLNPKMAEKDCYFIG 77
QY 88 FNETSLCKKLADGPFEEVFLFKLTTEFGKSVINVDVNMELLTKTLGWDIQBELNKLTKTH 147
DB 78 FNEETCLVKIITGLLEFEVYLYLQNRPFESSEBQARAVQMTKVLQFLQKAKNLDAIT 137
QY 148 YSPPKFDRGLLQGLKLVVRFHAFSYVLSAMEKFAQAVRVL 191

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Db 138 TPDPPTNASLLTKLQAOQWLMQDMMTHLILRSFKFLIRSLRAL 181

RESULT 7

ID ADL89593 standard; protein; 183 AA.

AC ADL89593;

XX 03-JUN-2004 (first entry)

DT Human modified cytokine protein #875.

DE Human; cytokine; proteolysis; interferon; IFN; interleukin-10; IL-10;
 XX long-chain cytokine family; short-chain cytokine family; infection;
 KW allergy; heart disease; cancer; liver disorder; autoimmune disease;
 KW growth disorder; diabetes; neurodegenerative disease; antimicrobial;
 KW antiallergic; cytostatic; immunosuppressive; antidiabetic;
 KW neuroprotective; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX W02004022593-A2.

XX 18-MAR-2004.

XX 08-SEP-2003; 2003WO-IB004347.

XX 09-SEP-2002; 2002US-0409898P.

XX 21-MAR-2003; 2003US-0457135P.

XX (NAUT-) NAUTILUS BIOTECH.

XX Gantier R, Guyon T, Vega M, Drittanti L;

XX WPI; 2004-248447/23.

XX New modified cytokines with increased resistance to proteolysis, useful
 PT for diagnosing and treating diseases such as infections, allergies, heart
 PT diseases, cancer, liver disorders, autoimmune diseases or diabetes.
 XX Disclosure; SEQ ID NO 927; 316pp; English.

XX The invention relates to modified cytokines that exhibit increased
 CC resistance to proteolysis compared to unmodified cytokines. The invention
 CC also relates to nucleic acid molecules encoding the cytokines, a
 CC pharmaceutical composition comprising a nucleic acid molecule in a
 CC molecule having a predetermined property or activity, or a pre-selected
 CC altered phenotype. The modified cytokine is selected from a member of the
 CC interferons (IFNs)/interleukin (IL)-10 protein family, a member of the
 CC long-chain cytokine family or a member of the short-chain cytokine
 CC family. The composition and method are useful for diagnosing and treating
 CC diseases such as infections, allergies, heart diseases, cancer, liver
 CC disorders, autoimmune diseases, growth disorders, diabetes or
 CC neurodegenerative diseases. This sequence represents a human modified
 CC cytokine protein of the invention.

XX Sequence 183 AA;

Query Match 17.0%; Score 186; DB 8; Length 183;
 Best Local Similarity 26.2%; Pred. No. 9.7e-13;
 Matches 43; Conservative 37; Mismatches 84; Indels 0; Gaps 0;

Qy 28 PEPEKLLIQLRNMLWVDECFRDLCYRTGICNGILEPAAIFHLKLPAINDDHCGLIG 87

Db 17 PLTSSERIDQIRVLDIGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCQFSQ 76

Qy 88 FNETSCLKLADGFEFFEVFLFKLTTEFGKSVINDVWELLTKLWDIOEEELNKLTKH 147

Db 77 FNETCLVKITITGLLEFEVLYLEQLNRFESSEQARAVQMSTKVLIQFLQKKARNLDAIT 136

Qy 148 YSPKFDRLGLLQGLKLYWRHFASFYVLNAMEKFAQAVRVL 191

Db 137 TSDPTTNASLLTKLQAOQWLMQDMMTHLILRSFKFLQSSRLAL 180

RESULT 8

AAW08477

ID AAW08477 standard; protein; 184 AA.

XX AAW08477;

XX 25-MAR-2003 (revised)

DT 24-FEB-1997 (first entry)

XX Interleukin-6 variant #2.

DE Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist;
 KW bovine; granulocyte colony stimulating factor; BG-CSF; receptor; gp130;
 KW thrombocytopaenia; haematopoietic progenitor cell; rheumatoid arthritis;
 KW bone marrow transplantation; gene therapy; multiple myeloma; leukaemia;
 KW breast cancer; infectious disease; bone marrow progenitor cell; therapy;
 KW postmenopausal osteoporosis; systemic lupus erythematosus; hormone.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 31 /note= "Y31D"

XX Misc-difference 35 /note= "G35P"

XX Misc-difference 74 /note= "F74Y"

XX Misc-difference 75 /note= "Q75Y"

XX Misc-difference 76 /note= "S76I"

XX Misc-difference 118 /note= "S118R"

XX Misc-difference 121 /note= "V121D"

XX Misc-difference 175 /note= "Q175I"

XX Misc-difference 176 /note= "S176R"

XX Misc-difference 183 /note= "Q183A"

XX W09618648-A1.

XX 20-JUN-1996.

XX 13-DEC-1995; 95WO-IT000216.

XX 14-DEC-1994; 94IT-RW000805.

XX (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.

XX Ciliberto G, Savino R, Lahm A, Toniatti C;

XX WPI; 1996-300575/30.

XX Identifying interleukin-6 super-agonists and (super)antagonists - using a
 PT 3-dimensional model of bovine granulocyte colony stimulating factor to
 PT identify binding sites.
 XX Claim 10; Page ?; 26pp; English.

XX AAW08476-W08478 represent human interleukin-6 (IL-6) mutants (see
 CC AAW02609 for wild type sequence), with greater affinity for the receptor,
 CC which can be used as IL-6 antagonists and superantagonists. These
 CC sequences were identified using the method of the invention. The method
 CC comprises comparing IL-6 with the bovine granulocyte colony stimulating
 CC factor (bG-CSF) sequence. On the basis of this comparison a 3-dimensional

model of IL-6 is formulated, which allows the identification of residues that form the site of interaction with the specific receptor, and those that constitute the site of interaction with gp130. The method can be used to identify superagonists, antagonists, and superantagonists of IL-6. The IL-6 superagonists identified by this method can be used for the treatment of thrombocytopaenia, and for the ex vivo expansion of human haematopoietic progenitor cells for bone marrow transplantation and gene therapy. They can also be used for the treatment of breast cancer, leukaemia, and infectious diseases or diseases connected with disorders of bone marrow progenitor cells. The antagonists and superantagonists identified by the method can be used for the treatment of diseases characterised by the overproduction of IL-6, particularly multiple myeloma, rheumatoid arthritis, postmenopausal osteoporosis, and systemic lupus erythematosus. The method can also be used to identify IL-6 variants with a greater affinity for the specific receptor (see AAW02610-W02612), or variants with a reduced or abolished affinity for gp130. (Updated on 25-MAR-2003 to correct PR field.)

Query Match 16.9%; Score 185.5; DB 2; Length 184;
Best Local Similarity 28.0%; Pred. No. 1.1e-12;
Matches 44; Conservative 31; Mismatches 71; Indels 11; Gaps 1;
Sequence 184 AA;
46 IDECFRDL-----CYRTGICKGILEPAAIFHLKLPALNDTHCGLIGENETSC 94
25 IDKIRDIIDFISLRKETCNKSNMCSSEKALAEENLNLPKMAEKDGYFIFGNEETCL 84
95 KKLADGFFFEVLKPLTFTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFD 154
85 VKIITGLLEFEVLYLQNRFFESSEBQARAVQVMTKDLQFLQKKAKNLDAITTPDPTN 144
155 RGLLGRLOGLKTVWRHFASFYVLSAMEKFAQAVRVL 191
145 ASLLTKLQANQLQDMTTHLILRSFKFLIRSLRAL 181

RESULT 9
ID ABP72702 standard; protein; 570 AA.
AC ABP72702;
DT 11-JUN-2003 (first entry)
DE Human interleukin-6-receptor isoform DS-sIL-6R fusion protein.
KW Human; interleukin-6; receptor; DS-sIL-6R; antibacterial; virucide;
KW anti-HIV; antirheumatic; antiarthritic; antinflammatory;
KW immunosuppressive; gene therapy.

Homo sapiens.
OS Synthetic.
OS Chimeric.
Key Location/Qualifiers
FT Protein 1..364
FT /label= DS-sIL-6R
FT Peptide 365..376
FT /label= Linker
FT Protein 377..560
FT /label= IL-6
FT Peptide 561..570
FT /label= C-myc tag

WO2003014359-A2.
XX
XX
PD 20-FEB-2003.
PD
PF 02-AUG-2002; 2002WO-GB003581.
XX
XX
PR 03-AUG-2001; 2001GB-00019015.
XX

(UYCA-) UNIV COLLEGE CARDIFF.
(UYWA-) UNIV WALES COLLEGE OF MEDICINE.
Jones SA, Topley N;
WPI; 2003-256588/25.
New fusion protein having a functional IL-6 and DS-sIL-6R molecule, useful for the manufacture of a medicament for the prophylaxis or treatment of an infectious disease, and an inflammatory or immunological disorder.
Disclosure; Fig 5; 46pp; English.
The present sequence is the protein sequence of a novel fusion protein comprising a soluble form of the human interleukin-6 receptor, denoted DS-sIL-6R (see also ABP72698), joined via a peptide linker to a human IL-6 molecule (see also ABP72700), with a C-terminal c-myc tag sequence.
Administration of this fusion protein results in the increased expression of one or more of MIP-1alpha, MIP-1beta, RANTES or IP-10. High levels of MIP-1alpha, MIP-1beta and RANTES complete with HIV for binding to CCR5 and effectively suppress HIV entry. The fusion protein can be used in the treatment of any disease in which the infectious agent binds to CCR5, especially M-trophic strains of HIV. The invention also provides a nucleic acid molecule encoding the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein in the host cell. The fusion protein, nucleic acid or vector can be used in the manufacture of a medicament for the prophylaxis or treatment of an infectious disease (especially AIDS caused by a M-trophic strain of HIV, or bacterial peritonitis), an inflammatory disorder or an immunological disorder (especially rheumatoid arthritis), when it is desirable to increase or resolve an immune response (claimed)

Query Match 16.9%; Score 185.5; DB 6; Length 570;
Best Local Similarity 25.9%; Pred. No. 5e-12;
Matches 49; Conservative 36; Mismatches 89; Indels 15; Gaps 2;
Sequence 570 AA;

18 SGTGKLPDAP--EFEKDLII-----QRLNMMLVVIDCFRDLCYRTGICKG 62
369 SGGGSLPVPVPGEDSKDVAAPHRQPLTSSERTDQIRVILDIGISLRKETCNKSNMCS 428
63 ILEPAAIFHLKLPALNDTHCGLIGNETSCILKLADGFFFEVLKPLTFTEFGKSVIN 122
429 SKEALAEENLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVLYLQNRFFESSEBQA 488
123 DVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLRLOGLKTVWRHFASFYVLSAMEK 182
489 RAVQVSTKVLQFLQKKAKNLDAITTPDPTTNASLLTKLQANQLQDMTTHLILRSFKE 548

183 FAGQAVRVL 191
549 FLQSSLRAL 557

RESULT 10
ID AAW08476 standard; protein; 184 AA.
XX AAW08476;
AC AAW08476;
XX
DT 25-MAR-2003 (revised)
DT 24-FEB-1997 (first entry)
XX
DE Interleukin-6 variant #1.

Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist;
KW bovine; granulocyte colony stimulating factor; BG-CSF; receptor; gp130;
KW thrombocytopaenia; haematopoietic progenitor cell; rheumatoid arthritis;
KW bone marrow transplantation; gene therapy; multiple myeloma; leukaemia;
KW breast cancer; infectious disease; bone marrow progenitor cell; therapy;
KW postmenopausal osteoporosis; systemic lupus erythematosus; hormone.

Matches	43;	Conservative	36;	Mismatches	85;	Indels	0;	Gaps	
Qy	28	PEFEKDLLIQRLNWMWLVIDEFCRDLCYRTGICKGILEPPAAIFHLKLPAINDTDHCGLTG	87						
Db	17	PLTSSRIDKQIRYILDIGISALRKETCNKSNWCESSKEALAENNLNLPKIAEKDGCFOG	76						
Qy	88	FNETSCLKKLADGPFEPFVFLFKFLTTERGKSVINVDVMELLTKTLGWDIOBELNKLTKTH	147						
Db	77	FNEETCLVKIITGLLEFEVYLEYLQNRFPESSEQARAVQMSTKVLQIQFKKAKNLDALT	136						
Qy	148	YSPKPFDRGLCRLOGLKXVWRHFPASFYVLSAMEKFAQAVRYL	191						
Db	137	TPDPTTNASLTLKQAQNWQLQDMTTHLILRSFKFLOSSLRAL	180						
RESULT 12									
ID	AAP81162 standard; protein; 201 AA.								
XX	AC	AAP81162;							
XX	AC								
DT	25-MAR-2003	(revised)							
DT	15-OCT-1990	(first entry)							
XX	Polypeptide with B-cell differentiation factor (BCDF) activity.								
XX	DE	B-cell differentiation factor; BCDF; cancer; autoimmune.							
XX	KW	Homo sapiens.							
XX	OS								
XX	PN	EP257406-A.							
XX	XX								
XX	XX	02-MAR-1988.							
XX	XX								
XX	XX	06-AUG-1987; 87EP-00111409.							
XX	XX								
XX	XX	06-AUG-1986; 86JP-00184858.							
XX	XX	27-AUG-1986; 86JP-00200433.							
XX	XX	18-DEC-1986; 86JP-00302699.							
XX	XX	13-MAY-1987; 87JP-00116332.							
XX	XX	16-NOV-1987; 87JP-00289007.							
XX	XX								
PA	(AJIN) AJINOMOTO KK.								
XX	XX	Kishimoto T, Hirano T, Matsui H, Takahara Y, Akiyama Y, Okano A;							
XX	PI								
XX	XX	WPI; 1988-057698/09.							
DR	XX								
PT	XX	Purified poly:peptide with B-cell differentiation factor activity -							
PT	XX	useful in prodn. of antibodies for diagnosis and therapy of cancers,							
PT	XX	infectious diseases etc.							
XX	XX								
PS	Claim 12;	Page 41; 72pp; English.							
XX	XX								
CC	XX	Peptide with BCDF activity may be used in the production and repair of B-							
CC	XX	cells, it is useful in treatment of autoimmune diseases, malignant tumors							
CC	XX	and may be used to influence B-cells to produce Abs in vitro. (Updated on							
CC	XX	25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR							
CC	XX	field.)							
XX	XX								
SQ	Sequence 201 AA;								
Query Match 16.8%; Score 184; DB 1; Length 201;									
Best Local Similarity 28.1%; Pred. No. 1.9e-12;									
Matches	41;	Conservative	31;	Mismatches	74;	Indels	0;	Gaps	
Qy	46	IDECFRDLCYRTGICKGILEPPAAIFHLKLPAINDTDHCGLTGICFNSTCLKKLADGFFBFE	105						
Db	53	IDKLKRETCNKSNCWCESSKEALAENNLNLPKMAEKDGCFOGCFNEETCLVKIITGLLEFE	112						
Qy	106	VLFPKLTTFTEFGKSVINVDVMELLTKTLGWDIOBELNKLTKTHSYPPKFDRLGLGRLOGLK	165						
Db	113	VLYEYLQNRFPESSEQARAVQMSTKVLQIQFKKAKNLDALTTPDPTTNASLTLKQAO	172						

CC arthritis, Kaposi sarcoma (associated with human immunodeficiency virus
CC infection, HIV), hypercalcaemia, bone disease, inflammatory disease,
CC stunted growth and systemic onset juvenile chronic arthritis. The methods
CC are useful for improving the efficiency and reliability in the discovery
CC and development of drugs and in the validation of IL6 as a drug target.
CC The antibody is useful in diagnostic, prognostic and therapeutic methods.
CC The IL6 isogene is useful in studying the expression and function of IL6,
CC and in expressing IL6 protein for use in screening for candidate drugs.
CC The gene for IL6 is located on chromosome 7p21-p15. The present sequence
CC is an interleukin-6 protein variant. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the IL6
CC sequence appearing as AAU99244 and the information on page 29
XX Sequence 212 AA;
SQ

Query Match 16.8%; Score 184; DB 5; Length 212;
Best Local Similarity 25.8%; Pred. No. 2e-12;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQLNMLWVDECFRDLCYRT 57
Db 16 LGLLLVLPAAFPAPVTPGEDSKDVAAPHROPPLTSSERIDKQIRYILDGIGALKRKTCKNS 75
Qy 58 GICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCCLKLADGFFFEVLFKFLTTFEGK 117
Db 76 NMCESSKEALAENNLNLPKMAEKDGCFCQSGFNEETCLVKITGLLEFEVLEYLQNRFS 135
Qy 118 SVINVDVMELLTKTLGWIDIOBELNKLTKTHYSPPKFDRGLLGRLOGLUKYVVRHFASPYVL 177
Db 136 SEEQARAVQMSKVLQFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDMTHLIL 195
Qy 178 SAMEKFAGQAVRVL 191
Db 196 RSPKEFLQSSLRAL 209

RESULT 14
AAU99249
ID AAU99249 standard; protein; 212 AA.
XX
AC AAU99249;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human interleukin-6, IL6, variant #5.
XX

KW Human; interleukin-6; IL6; myeloma; arthritis; CAD; Kaposi sarcoma;
KW coronary artery disease; inflammatory cytokine; hypercalcaemia;
KW bone disease; inflammatory disease; HIV;
KW human immunodeficiency virus infection; stunted growth; isogene;
KW systemic onset juvenile chronic arthritis; haplotype; genotype;
KW chromosome 7p21-p15; gene therapy; SNP; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Misc-difference 31
FT /note= "Wild-type Pro substituted by Thr"
FT
FT Misc-difference 162
FT /note= "Wild-type Asp substituted by Glu"
XX
XX WO200238586-A2.
PN
XX
PD 16-MAY-2002.
XX
PF 09-NOV-2001; 2001WO-US047077.
XX
XX 09-NOV-2000; 2000US-0247578P.
PR
PR 21-AUG-2001; 2001US-0313963P.
XX
XX (GENA-) GENAISANCE PHARM INC.
PA
XX Bentivegna SC, Bieglecki KM, Chew A, Denton RR, Lachowicz M;

PI Nandabalan K, Parks KB, Sausker EA;
XX WPI; 2002-519290/55.
XX
XX Genetic variants of interleukin-6 isogenes for improving efficiency and
XX reliability in drug development for treating myeloma, coronary artery
XX disease, arthritis and Kaposi sarcoma.
PS Claim 29; Page; 86pp; English.
XX
CC The invention relates to a polynucleotide comprising a first nucleotide
CC sequence (NS1) comprising a IL6 (interleukin-6, an inflammatory cytokine)
CC isogene selected from isogenes 1-11 and 13-18 given in the specification,
CC where each isogene comprises the regions of NS1 and is further defined by
CC the corresponding sequence of polymorphisms whose locations and
CC identities are defined in the specification (PS2-PS6, PS8 and PS10-PS17),
CC or a second nucleotide sequence (NS2) complementary to NS1.
CC Alternatively, the sequence comprises a coding sequence for an IL6
CC isogene. Also included are methods of haplotyping/ genotyping (and
CC predicting the haplotype/genotype) of the IL6 gene of an individual,
CC identifying an association between a trait and at least one haplotype or
CC haplotype pair of the IL6 gene, an isolated oligonucleotide for detecting
CC a polymorphism in the IL6 gene, a recombinant non-human organism (III)
CC transformed or transfected with the IL6 polynucleotide, an isolated
CC fragment of the IL6 isogene comprising at least 10 and containing one of
CC the identified single- nucleotide polymorphisms (SNP), an isolated
CC polypeptide (or fragment) comprising an amino acid sequence which is a
CC polymorphic variant of IL6, an isolated monoclonal antibody specific for
CC IL6, a computer system for storing and analysing polymorphism data for
CC the IL6 gene, and a genome anthology for the IL6 gene. The IL6
CC polymorphic variant is useful in screening for drugs targeting IL6 that
CC are useful for treating myeloma, coronary artery disease (CAD),
CC arthritis, Kaposi sarcoma (associated with human immunodeficiency virus
CC infection, HIV), hypercalcaemia, bone disease, inflammatory disease,
CC stunted growth and systemic onset juvenile chronic arthritis. The methods
CC are useful for improving the efficiency and reliability in the discovery
CC and development of drugs and in the validation of IL6 as a drug target.
CC The antibody is useful in diagnostic, prognostic and therapeutic methods.
CC The IL6 isogene is useful in studying the expression and function of IL6,
CC and in expressing IL6 protein for use in screening for candidate drugs.
CC The gene for IL6 is located on chromosome 7p21-p15. The present sequence
CC is an interleukin-6 protein variant. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the IL6
CC sequence appearing as AAU99244 and the information on page 29
XX
SQ Sequence 212 AA;
Query Match 16.8%; Score 184; DB 5; Length 212;
Best Local Similarity 25.8%; Pred. No. 2e-12;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQLNMLWVDECFRDLCYRT 57
Db 16 LGLLLVLPAAFPAPVTPGEDSKDVAAPHROPPLTSSERIDKQIRYILDGIGALKRKTCKNS 75
Qy 58 GICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCCLKLADGFFFEVLFKFLTTFEGK 117
Db 76 NMCESSKEALAENNLNLPKMAEKDGCFCQSGFNEETCLVKITGLLEFEVLEYLQNRFS 135
Qy 118 SVINVDVMELLTKTLGWIDIOBELNKLTKTHYSPPKFDRGLLGRLOGLUKYVVRHFASPYVL 177
Db 136 SEEQARAVQMSKVLQFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDMTHLIL 195
Qy 178 SAMEKFAGQAVRVL 191
Db 196 RSPKEFLQSSLRAL 209

RESULT 15
AAU99250
ID AAU99250 standard; protein; 212 AA.
XX
AC AAU99250;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM: protein - protein search, using sw model

Run on: March 30, 2005, 21:58:00 ; Search time 53.9731 Seconds
(without alignments)
282.148 Million cell updates/sec

Title: US-10-828-343-2

Perfect score: 1095

Sequence: 1 MCWFKLWSLLVSGSLVSGT.....GQAVRVLDSPDVTDPVHDK 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	204	3	US-09-230-637-25
2	1095	100.0	204	3	US-09-230-371A-26
3	992	90.6	185	3	US-09-122-443-16
4	992	90.6	185	4	US-09-558-089-16
5	992	90.6	185	4	US-09-558-087-16
6	992	90.6	185	4	US-09-558-474-16
7	183.5	16.8	184	2	US-08-945-529-12
8	183	16.7	185	1	US-07-918-181A-4
9	183	16.7	185	1	US-07-918-181A-8
10	183	16.7	185	1	US-08-231-575-4
11	183	16.7	185	1	US-08-231-575-8
12	183	16.7	185	5	PCT-US93-06928-4
13	183	16.7	185	5	PCT-US93-06928-8
14	183	16.7	212	1	US-08-792-0198-9
15	183	16.7	212	3	US-08-988-819-9
16	183	16.7	212	3	US-09-016-534-9
17	183	16.7	212	3	US-08-097-869-7
18	183	16.7	212	3	US-08-795-473B-6
19	183	16.7	212	3	US-09-230-637-45
20	183	16.7	212	3	US-09-155-941-1
21	183	16.7	212	3	US-09-230-371A-27
22	183	16.7	212	4	US-09-439-856-6
23	183	16.7	212	4	US-09-462-941-13
24	183	16.7	212	6	5510472-2
25	183	16.7	212	6	5510472-2
26	183	16.7	232	4	US-09-949-016-10315
27	182	16.6	184	2	US-08-693-182-2

28	182	16.6	184	2	US-09-008-482-2	Sequence 2, Appli
29	181	16.5	183	1	US-08-009-973-1	Sequence 1, Appli
30	181	16.5	184	1	US-08-567-047-2	Sequence 2, Appli
31	181	16.5	184	2	US-08-567-048-2	Sequence 2, Appli
32	181	16.5	184	6	5186931-1	Patent No. 5186931
33	181	16.5	184	6	5186931-1	Patent No. 5186931
34	181	16.5	185	1	US-07-632-070B-1	Sequence 1, Appli
35	181	16.5	185	1	US-07-918-181A-2	Sequence 2, Appli
36	181	16.5	185	1	US-07-918-181A-6	Sequence 6, Appli
37	181	16.5	185	1	US-08-231-575-2	Sequence 2, Appli
38	181	16.5	185	1	US-08-231-575-6	Sequence 6, Appli
39	181	16.5	185	1	US-08-246-427A-5	Sequence 5, Appli
40	181	16.5	185	2	US-08-716-317-7	Sequence 7, Appli
41	181	16.5	185	2	US-08-766-620-5	Sequence 5, Appli
42	181	16.5	185	5	PCT-US93-06928-2	Sequence 2, Appli
43	181	16.5	185	5	PCT-US93-06928-6	Sequence 6, Appli
44	181	16.5	185	6	5186931-2	Patent No. 5186931
45	181	16.5	185	6	5186931-2	Patent No. 5186931

ALIGNMENTS

RESULT 1

US-09-230-637-25

; Sequence 25, Application US/09230637

; Patent No. 6264958

; GENERAL INFORMATION:

; APPLICANT: Hayward, Gary

; APPLICANT: Nicholas, John

; APPLICANT: Hardwick, J. Marie

; APPLICANT: Reitz, Marvin

; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma

; FILE REFERENCE: 1107.78372

; CURRENT APPLICATION NUMBER: US/09/230, 637

; CURRENT FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: 60/022,591

; PRIOR FILING DATE: 1996-07-25

; PRIOR APPLICATION NUMBER: PCT US 97/12931

; PRIOR FILING DATE: 1997-07-24

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 25

; LENGTH: 204

; TYPE: PRT

; ORGANISM: Kaposi's sarcoma-associated herpes-like virus

US-09-230-637-25

Query Match 100.0%; Score 1095; DB 3; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.5e-123;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MCWFKLWSLLVSGSLVSGTRGKLPDAPFEKDLLIQRNLNMLWVIDECPDRDLCYRTGIC	60
Db	1	MCWFKLWSLLVSGSLVSGTRGKLPDAPFEKDLLIQRNLNMLWVIDECPDRDLCYRTGIC	60
Qy	61	KGILEPAAIFHLKLPAINDTDHGCLIGFNETSCCLKADGFFFEVLFKELTTFEGKSVI	120
Db	61	KGILEPAAIFHLKLPAINDTDHGCLIGFNETSCCLKADGFFFEVLFKELTTFEGKSVI	120
Qy	121	NVDVMELLTKTGWDIQEELNKLTTKTHYSPKFDRLGLRQGLKYVVRHFASFYVLSAM	180
Db	121	NVDVMELLTKTGWDIQEELNKLTTKTHYSPKFDRLGLRQGLKYVVRHFASFYVLSAM	180
Qy	181	EKFAGQAVRVLDSPDVTDPVHDK	204
Db	181	EKFAGQAVRVLDSPDVTDPVHDK	204

RESULT 2

US-09-230-371A-26

; Sequence 26, Application US/09230371A

; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; CURRENT FILING DATE: 1999-11-17
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-26

Query Match 100.0%; Score 1095; DB 3; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.5e-123;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLDGFFEFVLFKFLTFTEGKSVI 120
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QY 121 NVDMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRQLGKLYVVRHFPASFVYLSAM 180
DB 121 NVDMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRQLGKLYVVRHFPASFVYLSAM 180

QY 181 EKFAGQAVRVLSIPDVTDPVHDK 204
DB 181 EKFAGQAVRVLSIPDVTDPVHDK 204

RESULT 3
US-09-122-443-16
; Sequence 16, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-16

Query Match 90.6%; Score 992; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 7e-111;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 TRGKLPDAPPEFKDILLIQRNLNMLWVIDECFRDLCTRTGICKGILEPAAIFHLKLPAIND 79
DB 1 TRGKLPDAPPEFKDILLIQRNLNMLWVIDECFRDLCTRTGICKGILEPAAIFHLKLPAIND 60

QY 80 TDHCGLIGFNETSCLKKLDGFFEFVLFKFLTFTEGKSVINVDVWELLTKTLGWDIQEE 139
DB 61 TDHCGLIGFNETSCLKKLDGFFEFVLFKFLTFTEGKSVINVDVWELLTKTLGWDIQEE 120

QY 140 LNKLTHTHYSPPKFDGRLGRLGKLYVVRHFPASFVYLSAMEKFAQAVRVLSIPDVTTP 199
DB 121 LNKLTHTHYSPPKFDGRLGRLGKLYVVRHFPASFVYLSAMEKFAQAVRVLSIPDVTTP 180

QY 200 DVHDK 204
DB 181 DVHDK 185

RESULT 4
US-09-558-089-16
; Sequence 16, Application US/09558089
; Patent No. 6479634
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,089
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/122,443
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-089-16

Query Match          90.6%; Score 992; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 7e-111;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 80 TDHCGLIGFNETSCLKKLADGPFPEFVLFKPLTFTEFGKSVINVDVWMLLTKTGLGWDIQEE 139
Db 61 TDHCGLIGFNETSCLKKLADGPFPEFVLFKPLTFTEFGKSVINVDVWMLLTKTGLGWDIQEE 120

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Qy 200 DVHDK 204
Db 181 DVHDK 185

RESULT 5
US-09-558-087-16
; Sequence 16, Application US/09558087
; Patent No. 6495667
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/09/558,087
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-087-16

Query Match          90.6%; Score 992; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 7e-111;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 20 TRGKLPDAPEFEXDGLLIQRLNWMWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 79
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Qy 80 TDHCGLIGFNETSCLKKLADGPFPEFVLFKPLTFTEFGKSVINVDVWMLLTKTGLGWDIQEE 139
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Qy 140 LNKLTHTYSPKFDRLGLLQRLQGLKYWVRHFASFYVLSAMEKFAQAVRVLDSIPDVTP 199
Db 121 LNKLTHTYSPKFDRLGLLQRLQGLKYWVRHFASFYVLSAMEKFAQAVRVLDSIPDVTP 180

Qy 200 DVHDK 204
Db 181 DVHDK 185

RESULT 6
US-09-558-474-16
; Sequence 16, Application US/09558474
; Patent No. 6835825
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,474
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-474-16

Query Match          90.6%; Score 992; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 7e-111;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 TRGKLPDAPEFEXDGLLIQRLNWMWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 79
Db 1 TRGKLPDAPEFEXDGLLIQRLNWMWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 60

Qy 80 TDHCGLIGFNETSCLKKLADGPFPEFVLFKPLTFTEFGKSVINVDVWMLLTKTGLGWDIQEE 139
Db 61 TDHCGLIGFNETSCLKKLADGPFPEFVLFKPLTFTEFGKSVINVDVWMLLTKTGLGWDIQEE 120

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Query Match	16.7%;	Score 183;	DB 1;	Length 185;
Best Local Similarity	25.6%;	Pred. No. 1e-13;		

Matches	42;	Conservative	38;	Mismatches	84;	Indels	0;	Gaps	0;
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Db	79	FNEETCLVKIITGLLEFEVFLVLEQLNRFESSEEQARAVQMSTKVLIOFLQKKAKNLDAIT	138						
Qy	148	YSPKPFDRGLLGRLOGLKYWRHFASFVYLSAMEKPAQAVRVL	191						
Db	139	TPDPTTNASLLTKLQAQNWQLQDMTTHLIRSLKEFLQSSIRAL	182						
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; Sequence 4, Application PC/TUS9306928									
; GENERAL INFORMATION:									
; APPLICANT: Fowlkes, Dana M.									
; TITLE OF INVENTION: Carboxy Terminal IL-6 Muteins									
; NUMBER OF SEQUENCES: 35									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: InClone Systems Incorporated									
; STREET: 180 Varick Street									
; CITY: New York									
; STATE: New York									
; COUNTRY: U.S.A.									
; ZIP: 11014									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
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; PRIORITY APPLICATION DATA:									
; APPLICATION NUMBER: US 07/918,181									
; FILING DATE: 23-JUL-1992									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Feit, Irving N.									
; REGISTRATION NUMBER: 28,601									
; REFERENCE/DOCKET NUMBER: FOW-2-T									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: 212-645-1405									
; TELEFAX: 212-645-2054									
; INFORMATION FOR SEQ ID NO: 4:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 185 amino acids									
; TYPE: amino acid									
; TOPOLOGY: linear									
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/792,019B
; APPLICATION NUMBER: 31,602
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
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; LOCATION: -30..0
; US-08-792-019B-9

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Qy 178 SAMEKFAQAVRVL 191
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US-08-988-819-9
; Sequence 9, Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,819
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; NAME/KEY: Region
; LOCATION: -30..0
; US-08-988-819-9

Query Match 16.7%; Score 183; DB 3; Length 212;
Best Local Similarity 25.8%; Pred. No. 1.3e-13;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

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Db 76 NMCESSKEALAENNLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEPEVYLVYLNRFES 135
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Db 136 SEQARAVQMSKVLQIFLOKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTTHLIL 195
Qy 178 SAMEKFAQAVRVL 191
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: March 30, 2005, 21:49:40 ; Search time 172.897 Seconds
(without alignments)
390.664 Million cell updates/sec

Title: US-10-828-343-2
Perfect score: 1095
Sequence: 1 MCWFKUWLLVGLVSGT.....GQAVRVLDSPDVTDPVHDK 204

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	184	16.8	183	16	US-10-658-834A-901
3	183	16.7	183	16	US-10-658-834A-900
4	183	16.7	183	16	US-10-658-834A-918
5	183	16.7	183	16	US-10-658-834A-920
6	183	16.7	183	16	US-10-658-834A-928
7	183	16.7	212	9	US-09-854-280-14
8	183	16.7	212	9	US-09-854-208-14
9	183	16.7	212	14	US-10-099-007A-3
10	183	16.7	212	14	US-10-400-377-13
11	183	16.7	212	14	US-10-400-708-13
12	183	16.7	212	14	US-10-298-148-13
13	183	16.7	212	15	US-10-440-464-61

Sequence 13, Appl	14	183	16.7	212	16	US-10-773-939-13	Sequence 13, Appl
Sequence 13, Appl	15	183	16.7	212	16	US-10-774-149-13	Sequence 13, Appl
Sequence 13, Appl	16	183	16.7	212	17	US-10-685-288-13	Sequence 13, Appl
Sequence 906, App	17	182	16.6	183	16	US-10-658-834A-906	Sequence 906, App
Sequence 926, App	18	182	16.6	183	16	US-10-658-834A-926	Sequence 926, App
Sequence 198, App	19	181	16.5	183	16	US-10-658-834A-198	Sequence 198, App
Sequence 217, App	20	181	16.5	183	16	US-10-658-834A-217	Sequence 217, App
Sequence 898, App	21	181	16.5	183	16	US-10-658-834A-898	Sequence 898, App
Sequence 905, App	22	181	16.5	183	16	US-10-658-834A-905	Sequence 905, App
Sequence 908, App	23	181	16.5	183	16	US-10-658-834A-908	Sequence 908, App
Sequence 914, App	24	181	16.5	183	16	US-10-658-834A-914	Sequence 914, App
Sequence 917, App	25	181	16.5	183	16	US-10-658-834A-917	Sequence 917, App
Sequence 919, App	26	181	16.5	183	16	US-10-658-834A-919	Sequence 919, App
Sequence 921, App	27	181	16.5	183	16	US-10-658-834A-921	Sequence 921, App
Sequence 922, App	28	181	16.5	183	16	US-10-658-834A-922	Sequence 922, App
Sequence 925, App	29	181	16.5	183	16	US-10-658-834A-925	Sequence 925, App
Sequence 929, App	30	181	16.5	183	16	US-10-658-834A-929	Sequence 929, App
Sequence 939, App	31	181	16.5	183	16	US-10-658-834A-939	Sequence 939, App
Sequence 3, Appl	32	181	16.5	184	14	US-10-053-355A-3	Sequence 3, Appl
Sequence 134, App	33	181	16.5	185	16	US-10-872-198-134	Sequence 134, App
Sequence 163, App	34	181	16.5	186	14	US-10-083-446-163	Sequence 163, App
Sequence 163, App	35	181	16.5	186	17	US-10-948-576-163	Sequence 163, App
Sequence 10, Appl	36	181	16.5	190	15	US-10-311-473-10	Sequence 10, Appl
Sequence 145, App	37	181	16.5	317	14	US-10-083-446-145	Sequence 145, App
Sequence 145, App	38	181	16.5	317	17	US-10-948-576-145	Sequence 145, App
Sequence 12, Appl	39	181	16.5	807	15	US-10-311-473-12	Sequence 12, Appl
Sequence 1, Appl	40	180	16.4	166	14	US-10-246-946-1	Sequence 1, Appl
Sequence 899, App	41	180	16.4	183	16	US-10-658-834A-899	Sequence 899, App
Sequence 903, App	42	180	16.4	183	16	US-10-658-834A-903	Sequence 903, App
Sequence 907, App	43	180	16.4	183	16	US-10-658-834A-907	Sequence 907, App
Sequence 915, App	44	180	16.4	183	16	US-10-658-834A-915	Sequence 915, App
Sequence 923, App	45	180	16.4	183	16	US-10-658-834A-923	Sequence 923, App

ALIGNMENTS

RESULT 1

US-10-658-834A-927
; Sequence 927, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 927
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-927

Query Match 17.0%; Score 186; DB 16; Length 183;
Best Local Similarity 26.2%; Pred. No. 1.1e-12;
Matches 43; Conservative 37; Mismatches 84; Indels 0; Gaps 0;
Qy 28 PEFEKLLLTORLNMWLVDECFRDLCYRTGICKGILEPAAIFHLKLPAINDDHCLIG 87
Db 17 PLTSSRIDQRIYILDIGISALRKETCNKSNMCESSKEALAEANNLNPRAEKDGCPSQ 76
Qy 88 FNETSLKKLADGFFFEVLKFTTTEFGKSVINVDVMELLTKTLGWDIOELNKLTKTH 147

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Db 77 FNEETCLVKIITGLLEFEVYLVQNRFSSSEQARAVQMTKVLQFLQKKAKNLDATT 136
QY 148 YSPPKFDRGLLGRLOGLKYVWRHFPASFYVLSAMEKFAQAVRVL 191
Db 137 TSDPTTNASLLTKLQAQONQWLQDMTTHLILRSFKFQSSLRAL 180

RESULT 2
US-10-658-834A-901
; Sequence 901, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 901
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-901

Query Match 16.8%; Score 184; DB 16; Length 183;
Best Local Similarity 26.2%; Pred. No. 1.9e-12;
Matches 43; Conservative 36; Mismatches 85; Indels 0; Gaps 0;

QY 28 PEFKDLIIQRLNMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHGGLIG 87
Db 17 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKIAEKDGCFOG 76
QY 88 FNETSCLKKLADGPFPEVLFKFLTFTEFGKSVINVDVMELLTKTLGWDIOEELNKLTKTH 147
Db 77 FNEETCLVKIITGLLEFEVYLVQNRFSSSEQARAVQMTKVLQFLQKKAKNLDATT 136
QY 148 YSPPKFDRGLLGRLOGLKYVWRHFPASFYVLSAMEKFAQAVRVL 191
Db 137 TSDPTTNASLLTKLQAQONQWLQDMTTHLILRSFKFQSSLRAL 180

RESULT 3
US-10-658-834A-900
; Sequence 900, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 900
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-900

Query Match 16.7%; Score 183; DB 16; Length 183;
Best Local Similarity 25.6%; Pred. No. 2.5e-12;
Matches 42; Conservative 37; Mismatches 85; Indels 0; Gaps 0;

QY 28 PEFKDLIIQRLNMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHGGLIG 87
Db 17 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKVAEKDGCFOG 76
QY 88 FNETSCLKKLADGPFPEVLFKFLTFTEFGKSVINVDVMELLTKTLGWDIOEELNKLTKTH 147
Db 77 FNEETCLVKIITGLLEFEVYLVQNRFSSSEQARAVQMTKVLQFLQKKAKNLDATT 136
QY 148 YSPPKFDRGLLGRLOGLKYVWRHFPASFYVLSAMEKFAQAVRVL 191
Db 137 TSDPTTNASLLTKLQAQONQWLQDMTTHLILRSFKFQSSLRAL 180

RESULT 4
US-10-658-834A-918
; Sequence 918, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 918
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-918

Query Match 16.7%; Score 183; DB 16; Length 183;
Best Local Similarity 25.6%; Pred. No. 2.5e-12;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

QY 28 PEFKDLIIQRLNMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHGGLIG 87
Db 17 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFOG 76
QY 88 FNETSCLKKLADGPFPEVLFKFLTFTEFGKSVINVDVMELLTKTLGWDIOEELNKLTKTH 147
Db 77 FNEETCLVKIITGLLEFEVYLVQNRFSSSEQARAVQMTKVLQFLQKKAKNLDATT 136
QY 148 YSPPKFDRGLLGRLOGLKYVWRHFPASFYVLSAMEKFAQAVRVL 191
Db 137 TSDPTTNASLLTKLQAQONQWLQDMTTHLILRSFKFQSSLRAL 180

RESULT 5
US-10-658-834A-920
; Sequence 920, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
```

APPLICANT: Guyon, Thierry
APPLICANT: Dittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
PRIORITY FILING DATE: 2003-09-08
PRIORITY FILING DATE: 2003-03-21
PRIORITY FILING DATE: 2003-03-21
PRIORITY FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 920
LENGTH: 183
TYPE: PRT
ORGANISM: Homo sapiens
US-10-658-834A-920

Query Match 16.7%; Score 183; DB 16; Length 183;
Best Local Similarity 25.6%; Pred. No. 2.5e-12;
Matches 42; Conservative 37; Mismatches 85; Indels 0; Gaps 0;
QY 28 PFEKDLIQLRNWMLVDECFRDLCTGICKGILEPAAIFHLKLPAINDDTHCGLIG 87
DB 17 PLTSSRIDQIRYILDGIALRKETCNKSNMCESSKEALAENNLNPKMAEKDGCFSQ 76
QY 88 FNETSCLKLADGFFPEFVLKFLTFTEFGKSVINVDVWMLLTKYLGWDIOEELNKLTKTH 147
DB 77 FNEETCLVKIITGLLEFVYLVQNRFSSEQARAVQMSTKVLIQFLOKAKNLDIT 136
QY 148 YSPKPDRLGLRGLQGLKYVVRHFPASFYVLSAMEKEPAGQAVRVL 191
DB 137 TPDPTTNASLTKQAQNMQLDMTHLIILRSFKFLOSSLRAL 180

RESULT 6
US-10-658-834A-928
Sequence 928, Application US/10658834A
Publication No. US20040132977A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Dittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Acid
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
PRIORITY FILING DATE: 2003-09-08
PRIORITY FILING DATE: 2003-03-21
PRIORITY FILING DATE: 2003-03-21
PRIORITY FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 928
LENGTH: 183
TYPE: PRT
ORGANISM: Homo sapiens
US-10-658-834A-928

Query Match 16.7%; Score 183; DB 16; Length 183;
Best Local Similarity 25.6%; Pred. No. 2.5e-12;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;
QY 28 PFEKDLIQLRNWMLVDECFRDLCTGICKGILEPAAIFHLKLPAINDDTHCGLIG 87
DB 17 PLTSSRIDQIRYILDGIALRKETCNKSNMCESSKEALAENNLNPKMAEKDGCFSQ 76

QY 88 FNETSCLKLADGFFPEFVLKFLTFTEFGKSVINVDVWMLLTKYLGWDIOEELNKLTKTH 147
DB 77 FNEETCLVKIITGLLEFVYLVQNRFSSEQARAVQMSTKVLIQFLOKAKNLDIT 136
QY 148 YSPKPDRLGLRGLQGLKYVVRHFPASFYVLSAMEKEPAGQAVRVL 191
DB 137 TADPTTNASLTKQAQNMQLDMTHLIILRSFKFLOSSLRAL 180

RESULT 7
US-09-854-280-14
Sequence 14, Application US/09854280
Patent No. US20020052027A1
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Wood, William I.
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C2
CURRENT APPLICATION NUMBER: US/09/854,280
CURRENT FILING DATE: 2001-05-10
PRIORITY FILING DATE: US 09/311,832
PRIORITY FILING DATE: 1999-05-14
PRIORITY FILING DATE: US 60/085,579
PRIORITY FILING DATE: 1998-05-15
PRIORITY FILING DATE: US 60/113,621
PRIORITY FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 14
LENGTH: 212
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-280-14

Query Match 16.7%; Score 183; DB 9; Length 212;
Best Local Similarity 25.8%; Pred. No. 3e-12;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;
QY 12 VGSLLVSGTRGKLPDAP-EPEKDL-----LIQRLNMLWVDECFRDLCTYRT 57
DB 16 LGLLLVLPAPFAPVPFGEDSKDVAAPHROPLTSSRIDQIRYILDGIALRKETCNKS 75
QY 58 GICKGILEPAAIFHLKLPAINDDTHCGLIGFNETSCILKLDGFFPEFVLKFLTFTEGK 117
DB 76 NMCESSKEALAENNLNPKMAEKDGCFSQGNFETCLVKIITGLLEFVYLVQNRFS 135
QY 118 SVINVDVWMLLTKYLGWDIOEELNKLTKTHYSPKPDRLGLRGLQGLKYVVRHFPASFYVL 177
DB 136 SEQARAVQMSTKVLIQFLOKAKNLDITTPDPTTNASLTKQAQNMQLDMTHLIIL 195
QY 178 SAMEKFPAGQAVRVL 191
DB 196 RSFKEFLOSSLRAL 209

RESULT 8
US-09-854-208-14
Sequence 14, Application US/09854208
Patent No. US20020106743A1
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Wood, William I.
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: P1381-R1
CURRENT APPLICATION NUMBER: US/09/854,208

Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLWVIDECFRLCYRT 57
Db 16 LGLLLVLPAAFPAPVPPGDSKVAAPHROPILTSSERIDKQIRYILDGISALRKETCNKS 75
Qy 58 GICKGILEPAAIFHLKLPAINDDHCGLIGFNETSKLKLADGFFFEVLFKELTTFEGK 117
Db 76 NMCSSKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVLYLQNRFS 135
Qy 118 SVINVDVMELLTKTLGWDIOEELNKLTKTHYSPKPDRLGLLQGLKYVVRHFASFYVL 177
Db 136 SEEQARAVQMSKVLQFLOKKAENLDAITTPDPTTNASLLTKLQAOQNQLQDMTTHLIL 195
Qy 178 SAMEKFAQAVRVL 191
Db 196 RSPKEFLQSSLRAL 209

RESULT 12
US-10-298-148-13
; Sequence 13, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; TYPE: PRT
; LENGTH: 212
; ORGANISM: Homo sapiens
US-10-298-148-13

Query Match 16.7%; Score 183; DB 14; Length 212;
Best Local Similarity 25.8%; Pred. No. 3e-12;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;
Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLWVIDECFRLCYRT 57
Db 16 LGLLLVLPAAFPAPVPPGDSKVAAPHROPILTSSERIDKQIRYILDGISALRKETCNKS 75
Qy 58 GICKGILEPAAIFHLKLPAINDDHCGLIGFNETSKLKLADGFFFEVLFKELTTFEGK 117
Db 76 NMCSSKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVLYLQNRFS 135
Qy 118 SVINVDVMELLTKTLGWDIOEELNKLTKTHYSPKPDRLGLLQGLKYVVRHFASFYVL 177
Db 136 SEEQARAVQMSKVLQFLOKKAENLDAITTPDPTTNASLLTKLQAOQNQLQDMTTHLIL 195
Qy 178 SAMEKFAQAVRVL 191
Db 196 RSPKEFLQSSLRAL 209

RESULT 13
US-10-440-464-61
; Sequence 61, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SNOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE

; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-61

Query Match 16.7%; Score 183; DB 15; Length 212;
Best Local Similarity 25.8%; Pred. No. 3e-12;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;
Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLWVIDECFRLCYRT 57
Db 16 LGLLLVLPAAFPAPVPPGDSKVAAPHROPILTSSERIDKQIRYILDGISALRKETCNKS 75
Qy 58 GICKGILEPAAIFHLKLPAINDDHCGLIGFNETSKLKLADGFFFEVLFKELTTFEGK 117
Db 76 NMCSSKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVLYLQNRFS 135
Qy 118 SVINVDVMELLTKTLGWDIOEELNKLTKTHYSPKPDRLGLLQGLKYVVRHFASFYVL 177
Db 136 SEEQARAVQMSKVLQFLOKKAENLDAITTPDPTTNASLLTKLQAOQNQLQDMTTHLIL 195
Qy 178 SAMEKFAQAVRVL 191
Db 196 RSPKEFLQSSLRAL 209

RESULT 14
US-10-773-939-13
; Sequence 13, Application US/10773939
; Publication No. US20040175356A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/773,939
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-773-939-13

Query Match 16.7%; Score 183; DB 16; Length 212;
Best Local Similarity 25.8%; Pred. No. 3e-12;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;
Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLWVIDECFRLCYRT 57
Db 16 LGLLLVLPAAFPAPVPPGDSKVAAPHROPILTSSERIDKQIRYILDGISALRKETCNKS 75

QY 58 GICKGILEPAAIFHLKLPAINDTDHGGLIGFNETSCLKKLADGFFEFVLFKFLTTERGK 117
 Db 76 NNCSSKEALAENNLNLPMAEKDGCFOGFGNEETCLVKIITGLLEFEVYLEYLQNRRES 135
 QY 118 SVINVDVMBELLTKTGWDIQEELNKLTKTHYSPKPFDRGLGRLOGLKYVVRHFPASFYVL 177
 Db 136 SEEQARAVQMSTKVLQIQLQKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTTHLIL 195
 QY 178 SAMEKPAQAVRVL 191
 Db 196 RSFKEFLOSSRAL 209

RESULT 15
 US-10-774-149-13
 ; Sequence 13, Application US/10774149
 ; Publication No. US20040175800A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cox III, George N
 ; APPLICANT: Bolder Biotechnology, Inc.
 ; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
 ; FILE REFERENCE: 4152-1-PUS
 ; CURRENT APPLICATION NUMBER: US/10/774,149
 ; CURRENT FILING DATE: 2004-02-05
 ; PRIOR APPLICATION NUMBER: US/10/400,377
 ; PRIOR FILING DATE: 2003-03-26
 ; PRIOR APPLICATION NUMBER: US/09/462,941
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 60/052,516
 ; PRIOR FILING DATE: 1997-07-14
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 13
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ;
 US-10-774-149-13

Query Match 16.7%; Score 183; DB 16; Length 212;
 Best Local Similarity 25.8%; Pred. No. 3e-12;
 Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;
 QY 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNWMWVIDCFRDLCYRT 57
 Db 16 LGLLLVLPAAFPAPVPPGDSKDVAAPHRQPIVTSSEIDKQIRYILDGISAIRKETCNKS 75
 QY 58 GICKGILEPAAIFHLKLPAINDTDHGGLIGFNETSCLKKLADGFFEFVLFKFLTTERGK 117
 Db 76 NNCSSKEALAENNLNLPMAEKDGCFOGFGNEETCLVKIITGLLEFEVYLEYLQNRRES 135
 QY 118 SVINVDVMBELLTKTGWDIQEELNKLTKTHYSPKPFDRGLGRLOGLKYVVRHFPASFYVL 177
 Db 136 SEEQARAVQMSTKVLQIQLQKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTTHLIL 195
 QY 178 SAMEKPAQAVRVL 191
 Db 196 RSFKEFLOSSRAL 209

Search completed: March 30, 2005, 22:09:56
 Job time : 173.897 secs

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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:47:50 ; Search time 48.4843 Seconds
(without alignments)
404.837 Million cell updates/sec

Title: US-10-828-343-2

Perfect score: 1095

Sequence: 1 MCWFKLWSLLVGSLLVSGT.....GQAVRVLDSIPDTPDVHDX 204

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Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: piri:*

2: piri:*

3: piri:*

4: piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	180.5	16.5	212	2 I46590	interleukin 6 - pi
3	179.5	16.4	212	2 I46621	prointerleukin 6 -
4	173.5	15.8	208	2 T09216	interleukin-6 prec
5	150	13.7	208	1 S29549	interleukin-6 - sh
6	148	13.5	211	1 ICMS6	interleukin-6 prec
7	143.5	13.1	208	1 A56610	interleukin-6 prec
8	134	12.2	211	2 A34247	interleukin-6 prec
9	128	11.7	207	2 I46084	interleukin 6 - ca
10	92.5	8.4	873	2 E90581	hypothetical prote
11	86.5	7.9	408	2 H69472	coenzyme P420-quin
12	85	7.8	487	2 A56186	cyclin E - African
13	83	7.6	626	2 AG1256	DNA primase [impor
14	82.5	7.5	447	1 UBMBUM	tubulin beta-1 cha
15	82.5	7.5	449	2 QJ1589	tubulin beta-5 cha
16	82.5	7.5	969	2 T41707	probable pheromone
17	82	7.5	367	2 T18185	probable site-spec
18	82	7.5	636	2 AC1619	DNA primase [impor
19	81.5	7.4	442	2 S00683	tubulin beta-1 cha
20	80.5	7.4	449	2 QJ1591	tubulin beta-7 cha
21	80	7.3	874	2 AB0385	probable polyacch
22	80	7.3	955	2 F84372	valine-cRNA ligase
23	79.5	7.3	451	2 S50748	beta-tubulin - pot
24	79.5	7.3	452	2 S50748	beta-tubulin - pot
25	79.5	7.3	1017	2 S67804	LRG1 protein - yea
26	79	7.2	385	2 T27626	hypothetical prote
27	78.5	7.2	445	2 JA0048	tubulin beta-1 cha
28	78.5	7.2	674	2 T19495	hypothetical prote
29	77.5	7.1	609	2 S04757	NADH2 dehydrogenas

hypothetical prote
hypothetical prote
resistance protein
tubulin beta chain
tubulin beta chain
protein kinase - f
sarcosine oxidase
hypothetical prote
DNA-directed DNA p
DNA gyrase, chain
DNA gyrase subunit
probable rhoI GDP-
epididymal secreto
ABC transporter, A
hypothetical prote
cytochrome P450 2D

ALIGNMENTS

RESULT 1

IVHUB2

Interleukin-6 precursor [validated] - human

N;Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-cell on factor

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004

C;Accession: A32648; A25692; A26966; A3515; A25801; A25921; I52193; I56003; A27601; B27

R;Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muracani, K.; Matsuda, T.; Nakai, S.; Kishimoto

EMBO J. 6, 2939-2945, 1987

A;Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene

A;Reference number: A32648; MUID:88082664; PMID:3500852

A;Accession: A32648

A;Molecule type: DNA

A;Residues: 1-212 <YAS>

A;Cross-references: UNIPROT:P05231; GB:X00081; NID:G29494; PIDN:CAA68278.1; PID:G29495

A;Note: the authors translated the codon CAG for residue 130 as Glu

R;Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.

EMBO J. 5, 2529-2537, 1986

A;Title: Structure and expression of cDNA and genes for human interferon-beta-2, a disti

A;Reference number: A91051; MUID:87053818; PMID:3023045

A;Accession: A25692

A;Molecule type: mRNA

A;Residues: 1-212 <ZIL>

A;Cross-references: GB:X04430; NID:G32673; PIDN:CAA28026.1; PID:G32674

R;Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwamura

i, T.; Kishimoto, T.

Nature 324, 73-76, 1986

A;Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymphocy

A;Reference number: A93387; MUID:87065033; PMID:3491322

A;Accession: A26966

A;Molecule type: mRNA

A;Residues: 1-212 <HIR>

A;Cross-references: NID:G33849; PIDN:CAA28268.1; PID:G33850

R;Tonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.

Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989

A;Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization of

A;Reference number: A33515; MUID:89391958; PMID:2789513

A;Accession: A33515

A;Molecule type: mRNA

A;Residues: 1-212 <TON>

A;Cross-references: GB:M29150; NID:G186349; PIDN:AAA59154.1; PID:G307063

R;Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.

Eur. J. Biochem. 159, 625-632, 1986

A;Title: Structural analysis of the sequence coding for an inducible 26-kDa protein in h

A;Reference number: A25801; MUID:87004683; PMID:3758081

A;Accession: A25801

A;Molecule type: DNA; mRNA

A;Residues: 1-212 <HAE>

A;Cross-references: GB:X04403

A;Experimental source: fibroblast

R;May, L.T.; Helfgott, D.C.; Sehgal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A>Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; MUID:187067433; PMID:3538015
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAY>
 A:Cross-references: GB:M14584; NID:q184628; PIDN:AAA52728.1; PID:q306910
 R:Wong, G.G.; Witek-Giannotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 Behring Inst. Mitt. 83, 40-47, 1988
 A>Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
 A:Reference number: I52193; MUID:89193317; PMID:3266463
 A:Accession: I52193
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <WON>
 A:Cross-references: GB:M54894; NID:q186351; PIDN:AAC41704.1; PID:q186352
 R:Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A>Title: Molecular cloning and expression of hybridoma growth factor in *Escherichia coli*
 A:Reference number: I56003; MUID:88088768; PMID:3320204
 A:Accession: I56003
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <BRA>
 A:Cross-references: GB:M18403; NID:q184631; PIDN:AAA52729.1; PID:q306911
 R:Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A>Title: Separation and comparison of two monokines with lymphocyte-activating factor activity
 A:Reference number: A29816; MUID:88154445; PMID:3279116
 A:Accession: A27601
 A:Molecule type: protein
 A:Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VAN1>
 A:Accession: B27601
 A:Molecule type: protein
 A:Residues: 30-56, 'XX', 59-61, 'X', 63 <VA2>
 R:Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990
 A>Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved in cell growth and differentiation
 A:Reference number: A60400; MUID:90171574; PMID:2307841
 A:Accession: A60400
 A:Molecule type: protein
 A:Residues: 30-43 <YAM>
 R:Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A>Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and its cDNA
 A:Reference number: A29085; MUID:87092370; PMID:3491991
 A:Accession: A29085
 A:Molecule type: protein
 A:Residues: 29-42 <HIR2>
 R:Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Aizawa, H.
 Anticancer Res. 11, 961-968, 1991
 A>Title: Purification and characterization of human fibroblast derived differentiation factor
 A:Reference number: A61159; MUID:91290785; PMID:1640338
 A:Accession: A61159
 A:Molecule type: protein
 A:Residues: 30-42 <NOD>
 A:Experimental source: fibroblast
 R:Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A>Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor for human T cell leukemia cell lines
 A:Reference number: A61462; MUID:90121567; PMID:2610854
 A:Accession: A61462
 A:Molecule type: protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A>Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
 A:Reference number: A48419; MUID:91355644; PMID:1883960
 A:Accession: A48419
 A:Molecule type: protein
 A:Residues: 30-37, 'X', 39-40 <MAY2>
 A:Experimental source: FS-4 fibroblasts

A>Note: sequence extracted from NCBI backbone
 A>Note: this 28-30K form contained both N-linked and O-linked carbohydrate; a 25K form contained only N-linked carbohydrate
 A:Accession: C48419
 A:Molecule type: protein
 A:Residues: 28-40 <MAY3>
 A:Experimental source: FS-4 fibroblasts
 A>Note: sequence extracted from NCBI backbone (NCBIP:63787)
 A>Note: this 23-25K form contained O-linked but not N-linked carbohydrate
 R:Orlita, T.; Oneda, M.; Hasegawa, M.; Kuboniwa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A>Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 produced in *Escherichia coli*
 A:Reference number: JX0305; MUID:94266765; PMID:8206884
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R:Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A>Title: Disulfide structures of human interleukin-6 are similar to those of human granulocyte colony-stimulating factor
 A:Reference number: S04981; MUID:89286115; PMID:2472117
 A:Contents: annotation; disulfide bonds in recombinant protein
 R:Rock, F.L.; Li, X.; Chong, P.; Ida, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A>Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044; PMID:8172889
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factors and secreted. It therefore appears to function as an autoregulator of cell growth and differentiation.
 C:Comment: This protein plays a regulatory role in various host defense mechanisms and in hematopoiesis.
 A:Gene: GDB:IL6
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Introns: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growth factor; interleukin-6; signal sequence; status predicted <SIG>
 F:1-27/Domain: signal sequence; status predicted <SIG>
 F:28-212/Product: interleukin-6, long form; status experimental <MATL>
 F:30-212/Product: interleukin-6, short form; status experimental <MATS>
 F:72-78, 101-111/Disulfide bonds: #status experimental
 F:73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F:166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
 F:172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	16.7%	Score 183;	DB 1;	Length 212;
Best Local Similarity	25.8%	Pred. No. 5.5e-10;		
Matches	50;	Conservative 38;	Mismatches 9;	Indels 14;
Gaps	2;			

QY	12	VGSLVSGTRGKLPDAP-EFEKDL-----LIQRINMWLWVIDSCFRDLCYRT	57
		: : : : :	: : : : :
Db	16	LGLLVLPAPFAPVPPGEDSKVAAPHRQPLTSSRIDKQIRYILDGIALRKETCNKS	75
		: : : : :	: : : : :
QY	58	GICKGILEPAAIFHLKLPAINDTDHCGLIGNETSCLKLADGFEFEVLPKFLTFEGK	117
		: : : : :	: : : : :
Db	76	NMCSSKALANNLNLPMAEKDGCFOSGFNEETCLVKIITGLLEFEVLYEYLQNRPE	135
		: : : : :	: : : : :
QY	118	SVINVDVMEILLTKLGWDIQBELNKLTKTHYSPPKFDGGLGRQLGKLVVRRHFAFVYL	177
		: : : : :	: : : : :
Db	136	SEEQARAVQMSTKVLQFLQKKAKNLDAITTPDPTTNASLLTKLQAOQNQLQDWTHTLL	195
		: : : : :	: : : : :
QY	178	SAMEKFAQAVRVL	191
		: : : : :	: : : : :
Db	196	RSFKEFLQSRLAL	209

RESULT 2
 I46590
 Interleukin 6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 R:Mathialagan, N.; Bixby, J.; Roberts, M.R.
 Mol. Reprod. Dev. 32, 324-330, 1992
 A>Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conceptuses
 A:Reference number: I46590; MUID:92360284; PMID:1497880
 A:Accession: I46590

A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-212 <MAT>
A;Cross-references: UNIPROT:P26893; GB:M80258; NID:g164514; PIDN:AAC27127.1; PID:g164515
C;Genetics:
A;Gene: IL-6
C;Superfamily: interleukin-6

Query Match 16.4%; Score 180.5; DB 2; Length 212;
Best Local Similarity 23.9%; Pred. No. 9.5e-10;
Matches 47; Conservative 46; Mismatches 87; Indels 17; Gaps 2;

QY 12 VGSLLVSGTRGKLPDAPEFE-----KDLIIQLRLNMLWVIDECFRDLCYRT 57
Db 16 LGULLVMATAPPTPERLEEDAKGSDKMLFTSPDKTEELIKYILKISAMRKEMCEKY 75

QY 58 GICKGILEPAAIFHLKLPAINDTDHCGILGFNETSCCLKLADGFFEFVLFKLTTFEGK 117
Db 76 EKCEKSEKVLAEENNLNLPKMAEKDGCFCQSGFNQETCLMRITTTGLVFEQIYLDYLOKEYES 135

QY 118 SVINVDVWELLTKTLGWDIOEELNKLTKTHYSPPKFDRGLLGRLOGLKYVVRHFASFYVL 177
Db 136 NKGNEAVQISTKALIQTLAQKGNPKDKATTPNPTTNAGLLDKLQSQNEWMKNTKIIL 195

QY 178 SAME---KFAQQAVRVL 191
Db 196 RSLDFLQFSRAIRIM 212

RESULT 3
146621
prointerleukin 6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46621
R;Richards, C.; Saklatva, J.
Cytokine 3, 269-276, 1991
A;Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of
A;Reference number: I46621; MUID:91338547; PMID:1873476
A;Accession: I46621
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-212 <RIC>
A;Cross-references: UNIPROT:P26893; GB:M86722; NID:g164624; PIDN:AAC37333.1; PID:g164625
C;Genetics:
A;Gene: IL6
C;Superfamily: interleukin-6

Query Match 16.4%; Score 179.5; DB 2; Length 212;
Best Local Similarity 23.9%; Pred. No. 1.2e-09;
Matches 48; Conservative 49; Mismatches 79; Indels 25; Gaps 4;

QY 12 VGSLLVSGTR---GKLPD-----APFEKDLLIQLRLNMLWVIDECFRDL 53
Db 16 LGULLVMATAPPTPERLEEDAKGSDKMLFTSPDKTEEL---IKYILKISAMRKEM 71

QY 54 CYRTGICKGILEPAAIFHLKLPAINDTDHCGILGFNETSCCLKLADGFFEFVLFKLT 113
Db 72 CEKYEKSEKVLAEENNLNLPKMAEKDGCFCQSGFNQETCLMRITTTGLVFEQIYLDYLOK 131

QY 114 EFKSVINVDVWELLTKTLGWDIOEELNKLTKTHYSPPKFDRGLLGRLOGLKYVVRHFAS 173
Db 132 EYESKGNVEAVQISTKALIQTLRQKGNPKDKATTPNPTTNAGLLDKLQSQNEWMKNTKI 191

QY 174 FYVLSAME---KFAQQAVRVL 191
Db 192 ILILRSLEDFLQFSRAIRIM 212

RESULT 4
T09216
interleukin-6 precursor - horse
C;Species: Equus caballus (domestic horse)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09216
R;Swiderski, C.E.; Horohov, D.W.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z16613
A;Accession: T09216
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-208 <SWI>
A;Cross-references: UNIPROT:Q95181; EMBL:U64794; NID:g2654387; PID:g2654388
C;Genetics:
A;Gene: IL-6
C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor

Query Match 15.8%; Score 173.5; DB 2; Length 208;
Best Local Similarity 26.0%; Pred. No. 4.3e-09;
Matches 51; Conservative 37; Mismatches 89; Indels 19; Gaps 5;

QY 12 VGSLLVSGTRGKLP-----DAPEFEKDLII-----QLNMLWVIDECFRDLCYRTGIC 60
Db 16 LGULLVMATAPPTPLGDEDETTSGPFLTTADTKQHVKYILGKISALKNEMCNFSKC 75

QY 61 KGLEPAAIFHLKLPAINDTDHCGILGFNETSCCLKLADGFFEFVLFKLTTFEGKSVI 120
Db 76 ENSKEVLAENNLNLPKMAEKDGCFCQSGFNQETCLMKITTTGLSEFQIYLYLQNEFKGEKE 135

QY 121 NVDVWELLTKTLGWDIOEELNKLTKTHYS--PKFDRGLLGRLOGLKYVVRHFASFYVLS 178
Db 136 NIKTMQISTKVL---VOILMQKNPEVTTPDTAKSSLLAKLHSONEWLKNKTTTHLILR 192

QY 179 AME---KFAQQAVRVL 191
Db 193 SLEDFLQFSRAIRIM 208

RESULT 5
S29549
interleukin-6 - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S29549
R;Ebrahim, B.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29549
A;Accession: S29549
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-208 <EBR>
A;Cross-references: UNIPROT:P29455; EMBL:X68723
C;Superfamily: interleukin-6

Query Match 13.7%; Score 150; DB 1; Length 208;
Best Local Similarity 27.0%; Pred. No. 7.7e-07;
Matches 38; Conservative 28; Mismatches 71; Indels 4; Gaps 1;

QY 51 RDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGILGFNETSCCLKLADGFFEFVLFKF 110
Db 69 KEICEKNDCEKSEKVLAEENNLNLPKMAEKDGCFCQSGFNQAVCLITTAGLLBYQIYLDP 128

QY 111 LTTEFGKSVINVDVWELLTKTLGWDIOEELNKLTKTHYSPPKFDRGLLGRLOGLKYVVRH 170
Db 129 LQNEPEGNQETVMELQSSIRTLIQLKEKIAGLIIT---PATHTDLLEKMQSSNEWVKN 184

QY 171 FASFYVLSAMEKFAQQAVRVL 191
Db 185 AKVILIIRSLLENFLQFRLRAI 205

RESULT 6
ICMS6
interleukin-6 precursor - mouse
N;Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatoc

acytoma growth factor
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
 C:Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799; S10
 R:Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
 J. Immunol. 141, 3875-3881, 1988
 A:Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential
 A:Reference number: A30531; MUID:89035525; PMID:3263439
 A:Accession: A30531
 A:Molecule type: DNA
 A:Residues: 1-211 <TAN>
 A:Cross-references: UNIPROT:P08505; GB:M20572; NID:g198369; PIDN:AAA39302.1; PID:g387386
 R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.; Sim
 Eur. J. Immunol. 18, 193-197, 1988
 A:Title: cDNA cloning of murine interleukin-HP1: homology with human interleukin 6.
 A:Reference number: A27610; MUID:88166883; PMID:2965020
 A:Accession: A27610
 A:Molecule type: mRNA
 A:Residues: 1-211 <VAN>
 A:Cross-references: GB:X06203; NID:g52701; PIDN:CAA29560.1; PID:g52702
 R:Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Cla
 J. Immunol. 142, 1372-1376, 1989
 A:Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
 A:Reference number: A30571; MUID:89124383; PMID:2563387
 A:Accession: A30571
 A:Molecule type: mRNA
 A:Residues: 5-211 <MOC>
 A:Cross-references: GB:M24221; NID:g341131; PIDN:AA68814.1; PID:g870699
 R:Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
 Eur. J. Biochem. 176, 187-197, 1988
 A:Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and
 A:Reference number: S01323; MUID:88229059; PMID:3262059
 A:Accession: S01323
 A:Molecule type: protein
 A:Residues: 25-166, 'X', 168-211 <SIM>
 A:Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
 R:Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
 Nucleic Acids Res. 18, 6455, 1990
 A:Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
 A:Reference number: S12103; MUID:91057159; PMID:2243807
 A:Accession: S12103
 A:Molecule type: mRNA
 A:Residues: 1-211 <GRE>
 A:Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728
 R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
 Biochem. Biophys. Res. Commun. 166, 139-145, 1990
 A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
 A:Reference number: A90157; MUID:90147691; PMID:2302197
 A:Accession: E34047
 A:Molecule type: protein
 A:Residues: 66-69, 'X', 71-75; 78-94; 128-148 <JAS>
 R:Van Snick, J.; Cayphas, S.; Vink, A.; Uyttenhove, C.; Coulie, P.G.; Rubira, M.R.; Simp
 Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
 A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokin
 A:Reference number: A26662; MUID:87092311; PMID:2948184
 A:Accession: A26662
 A:Molecule type: protein
 A:Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
 R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
 A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clon
 A:Reference number: A40486; MUID:89017145; PMID:3262872
 A:Accession: A40486
 A:Molecule type: mRNA
 A:Residues: 1-211 <CHI>
 A:Cross-references: GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410
 R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
 Blood 72, 2070-2073, 1988
 A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6
 A:Reference number: A60799; MUID:89062753; PMID:3264198
 A:Accession: A60799
 A:Molecule type: protein
 A:Residues: 77-98 <SHA>

R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
 J. Exp. Med. 171, 965-970, 1990
 A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a mol
 A:Reference number: S10241; MUID:90171860; PMID:2106569
 A:Accession: S10241
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-6 <BLA>
 A:Cross-references: EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g5981860
 R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
 Eur. J. Biochem. 217, 53-59, 1993
 A:Title: Specific covalent modification of the tryptophan residues in murine interleukin-
 A:Reference number: S38254; MUID:94039075; PMID:8223586
 A:Accession: S38254
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 38-60; 75, 'X', 77-79; 176-203 <ZHA>
 C:Genetics:
 A:Gene: IL-6
 A:Map position: 5
 A:Introns: 7/1, 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; a
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 Query Match 13.5%; Score 148; DB 1; Length 211;
 Best Local Similarity 24.5%; Pred. No. 1.2e-06;
 Matches 47; Conservative 35; Mismatches 96; Indels 14; Gaps 3;
 QY 12 VGSLLVSGT-----RGKL-----PDAPFEKDLIIQRLNMLWVIDECFRDLCYRTG 58
 DB 15 LGLMLVTTTAPTTSQVRGDFTEPTNRPVYTSQVGLITHVLWEIVMRKELCNGNS 74
 QY 59 ICKGILEPAAIFHLKLPAINDTDHGILGFNETSLCKKLADGPFEPFVFLFKPLTFE-CK 117
 DB 75 DQNNDDALAENLKLPEIQNRDGCYQGYNQELCKLISKSSGLLEYHSYLEYMKNNLKD 134
 QY 118 SVINVDVWELLTKTLGWIDIQSELNKLTKTHYSPKFDRLGLGRLOGLKXVVRHFPASFVYL 177
 DB 135 KDKARVLQRTDTETLIHFNQEVKDLHKVILPTFISNALLTDKLSQKEWLRTKTIQFIL 194
 QY 178 SAMEKFAQAVR 189
 DB 195 KSLBEFLKVTLR 206
 RESULT 7
 A56610
 Interleukin-6 precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A56610; S22162
 R:Droogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
 DNA Seq. 2, 411-413, 1992
 A:Title: Nucleotide sequence of bovine interleukin-6 cDNA.
 A:Reference number: A56610; MUID:93076003; PMID:1446077
 A:Accession: A56610
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-208 <DRO>
 A:Cross-references: UNIPROT:P26892; EMBL:X57317; NID:g2193; PIDN:CAA40572.1; PID:g2194
 A:Experimental source: BLV induced B cell-lymphosarcoma
 A:Note: sequence extracted from NCBI backbone (NCBI:118917)
 C:Superfamily: interleukin-6
 C:Keywords: cytokine
 Query Match 13.1%; Score 143.5; DB 1; Length 208;
 Best Local Similarity 24.4%; Pred. No. 3.2e-06;
 Matches 42; Conservative 37; Mismatches 86; Indels 7; Gaps 2;
 QY 20 TRGKLDPAPFEKDLIIQRLNMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 79

Db 41 TPGRLTTTPEKTEALIKR---WVDKISAMRKEICEKNDECESSKETLAENKLNLPWEE 97

Qy 80 TDHCGLIGFNETSCLKKLADGFEFEVLKFLTEFGKSVINVDVWELLTKTLGWIDQEE 139

Db 98 KDGCFQSGFNAQICLIRTTAGLLEYQIYLDYQNEYEGNQENVRDLRKNIRTLIQLKQK 157

Qy 140 LNKLTHTHSPKFDRLGRLGLQKLYVVRHFAFYVLSAMEKFAQAVRL 191

Db 158 IADLITT---PATNTDLLEKMOSSNEWVKNKAIILIRNLLENFLQFSLRAI 205

RESULT 8

A34247

Interleukin-6 precursor - rat

N;Alternate names: IL-6

C;Species: Rattus norvegicus (Norway rat)

C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004

C;Accession: A34247

R;Northmann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.

J. Biol. Chem. 264, 16072-16082, 1989

A;Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derivative

A;Reference number: A34247; MUID:89380206; PMID:2789217

A;Accession: A34247

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-211 <NOR>

A;Cross-references: UNIPROT:P20607; GB:M26744; NID:g204915; PIDN:AAA77659.1; PID:g204916

C;Superfamily: interleukin-6

C;Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match 12.2%; Score 134; DB 2; Length 211;

Best Local Similarity 23.7%; Pred. No. 2.6e-05;

Matches 47; Conservative 34; Mismatches 91; Indels 26; Gaps 4;

Qy 12 VGSLLVSGT-----RGKLPDAPPEFKLLIQR-----DFTEDTHNRPVYTSQVGLITYVLRILEMRKE 52

Db 15 LGLMLLTATAPPTSQVRRG-----DFTEDTHNRPVYTSQVGLITYVLRILEMRKE 68

Qy 53 LCYRTGICKGILEPAAIFHLKLPAINDTDHGGLIGFNETSCLKKLADGFEFEVLKFLT 112

Db 69 LCNGNSDCMSDDALSNNLKLPEIQNDGCFQTYGNOEICLLKICSGLLEFRFYLEFVK 128

Qy 113 TEF-GKSVINVDVWELLTKTLGWIDQIELNKLTKHTHSPKFDRLGRLGLQKLYVVRHF 171

Db 129 NNLDQNKDKARVIQNSNTELVHIFKQIKDSYKIVLPTPTSNALLMEKLESQEWLRTK 188

Qy 172 ASFVLSAMEKFAQAVR 189

Db 189 TIQLIKALBEFLKVTWR 206

RESULT 9

I46084

Interleukin 6 - cat

C;Species: Felis silvestris catus (domestic cat)

C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C;Accession: I46084

R;Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.

Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993

A;Title: Molecular cloning and characterization of a cDNA encoding feline interleukin-6

A;Reference number: I46084; MUID:94052249; PMID:8234373

A;Accession: I46084

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-207 <BRA>

A;Cross-references: UNIPROT:P41683; GB:L16914; NID:g438519; PIDN:AAA16620.1; PID:g438520

C;Superfamily: interleukin-6

Query Match 11.7%; Score 128; DB 2; Length 207;

Best Local Similarity 27.8%; Pred. No. 9.7e-05;

Matches 42; Conservative 29; Mismatches 62; Indels 18; Gaps 5;

Qy 4 FKLMSLLLV-----GSLLVSGTRGKLPDAPPEFKLLIQLRLNMLWVIDECFRDLICYR 56

Db 14 FSIGLLLVWATAPPTPGPLGGDATSNRLPLTP---ADKMEELIKYILGKISALKKEMCDN 70

Qy 57 TGICKGILSPAALFHLKLPAINDTDHGGLIGFNETSCLKKLADGFEFEVLKFLTTEF- 115

Db 71 YNKCEDSKEALAEANNLNLKLAEDKCGFQSGFQNETCLIRITTTGLQEFQIYLFQLQDKYE 130

Qy 116 -----GKSV-INVDVWELLTKTLGWIDQIEL 140

Db 131 GDKENAKSVYVTSNVLQLMLKRGKGN-QDEV 160

RESULT 10

E90581

hypothetical protein MYPU_5570 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C;Species: Mycoplasma pulmonis

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: E90581

R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis

A;Reference number: A99512; MUID:21267165; PMID:11353084

A;Accession: E90581

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-873 <KUR>

A;Cross-references: UNIPROT:Q98Q12; GB:AL445566; PID:g14089972; PIDN:CAC13730.1; GSPDB:G13730.1

A;Experimental source: strain UAB CTIP

C;Genetics:

A;Gene: MYPU_5570

A;Genetic code: SGC3

C;Superfamily: alanyl-tRNA ligase

Query Match 8.4%; Score 92.5; DB 2; Length 873;

Best Local Similarity 24.3%; Pred. No. 1.3;

Matches 50; Conservative 27; Mismatches 58; Indels 61; Gaps 9;

Qy 32 KDLIIQLRLNMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHGGLIGFNET 91

Db 305 RDYIIRRL-----IRRAYRTGIQLGKDEAFLYKL-VPVIKDS---LIFDYDT 348

Qy 92 SCLKKLADGFEFEVLKFLTEFEFGKSVINVDVWELLTKTLGWIDQI----- 137

Db 349 ---KHVAKVIKDELLFESKTIQDGKKILEKFEKSKKIDASIVFRMPDTTGYVPELTKE 405

Qy 138 -----EELNKLTKHTHSPKFDRG-----LLGRLQGLKLYVVRHFAFYVLSAMEKFAQAVR 177

Db 406 AKEKGVEISLEEFKRYQHEHLSKSKKGDGMKVINFLANIDKKVDFVGYDTLETTSK 465

Qy 178 -----SAMEKFAQAVRVLDSIP 195

Db 466 ILYLFNSESKLNKLEGQYFILDKTP 491

RESULT 11

H69477

coenzyme F420-quinone oxidoreductase (EC 1.6.5.-) 53.9K chain AF1825 [similarity] - Arch.

N;Alternate names: F420H2-quinone oxidoreductase, 53.9K subunit nuoM homolog

C;Species: Archaeoglobus fulgidus

C;Date: 03-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: H69477

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: H69477

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-487 <KLE>

A;Cross-references: UNIPROT:Q28450; GB:AE000976; GB:AE000782; NID:g2689299; PIDN:AAB8942
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: oxidoreductase

Query Match 7.9%; Score 86.5; DB 2; Length 487;
Best Local Similarity 21.4%; Pred. No. 2.4;
Matches 48; Conservative 40; Mismatches 79; Indels 57; Gaps 12;

QY 4 FKLWILLVGSLLVSGTRGKLP-----DAFEFKDLL-----IQRLNML---- 43
Db 209 FTAWLLIFGLMLV-----KLPGLGPHIWLPAWAHAETPVSAALLSPLTVGLAGYVLLRV 262

QY 44 WVIDECF-----RDLCVRTGICKGILEPAAIFHLKLPAINDTDHGCLIGFNETS----- 92
Db 263 YMIDSSFDIQVRDIIIAIVSSIVAGFSVKQK-----DYKRLAYSTVSQGYVLI 315

QY 93 --CLKKLADGPFEPFVLFPKFLTTTEFGKSVINVDVNMELTKITLGMIDIOBELNKLTKTH--YS 149
Db 316 ALCL-----GSYGLGVVIQYISHAFGKSLFTWAGAIITASFHG---LRDINRMGMEYV 368

QY 150 PKFDRGLLG--RLGLKYWVRHFASFVLSAMEKFAQAVRVL 191
Db 369 PTIANAALLIGFTLSGI-LTIGMFGFYILAGLTTIYGFNLAVI 411

RESULT 12
A56186
Cyclin E - African clawed frog
N;Alternate names: cyclin E1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 12-Jul-2004
C;Accession: A56186; S34125
R;Rempel, R.E.; Sleight, S.B.; Maller, J.L.
J. Biol. Chem. 270, 6843-6855, 1995
A;Title: Maternal Xenopus Cdk2-cyclin E complexes function during meiotic and early embryonic development
A;Reference number: A56186; MUID:95204484; PMID:7896832
A;Accession: A56186
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-408 <REM>
A;Cross-references: UNIPROT:Q91780; GB:L23857; NID:g431745; PIDN:AAA73524.1; PID:g431746
R;Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, June 1992
A;Description: Cloning and expression of Xenopus cyclin E.
A;Reference number: S34125
A;Accession: S34125
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-32, 'A', 34-199, 'NV', 202-258, 'GN', 261-408 <COU>
A;Cross-references: EMBL:Z13966
C;Superfamily: cyclin, A/B/D/E type
C;Keywords: cell cycle control

Query Match 7.8%; Score 85; DB 2; Length 408;
Best Local Similarity 23.9%; Pred. No. 2.8;
Matches 37; Conservative 29; Mismatches 41; Indels 48; Gaps 10;

QY 28 PFEXKDLIQRLLNMLWVIDECFRDLCYRTGIC----KGILEPAAIFHLKLPAINDTDHC 83
Db 267 PQPQEQEIVQ----IVQLLDLCVLDIC-----CLBVPYGVLAASAMVHFSCELVK--- 314

QY 84 GLIGNET---SCLKKLADGPFEPFVLFPKFLTTEFGKSVIN-----VDV----- 124
Db 315 -VSGFKVTELOQCIKWL-----VPFAMATKEGKGKLNFPKFGVDIEDAHNIQTHSGC 365

QY 125 MELLTKT-LGWDIOBELNKLTKTH---YSPPKFDR 155
Db 366 LELMEKVINQALLBEQNETSPIPTGVLTTPQSNK 400

RESULT 13
AG1256
DNA primase [imported] - Listeria monocytogenes (strain EGD-e)

A;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG1256
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1256
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-626 <GLA>
A;Cross-references: UNIPROT:P47762; GB:NC_003210; PIDN:CAC99533.1; PID:g16410884; GSPDB:C
C;Genetics:
A;Gene: dnaG

Query Match 7.6%; Score 83; DB 2; Length 626;
Best Local Similarity 23.8%; Pred. No. 7;
Matches 41; Conservative 21; Mismatches 52; Indels 58; Gaps 8;

QY 13 GSLIVSGTR-----GKLPD-----APE-FEKDLIIQRLLNMLWVIDECFRDLCY 55
Db 327 GTLLVERNLDFVLQLPAGKOPDDFIRASGPEKEFVKQORWTWTAFKHYLKERNL 386

QY 56 RTGICKGILEPAAIFHLKLPAINDTDHGCLIGFNETSCLKKLA--DGFFEFEVLFPKFLTT 113
Db 387 Q-----NETEQIGYI---DDCLREIAKLDAQVERELYKQLAD 421

QY 114 EFGKSVINVDVNMELTKITLGMIDIOBELNKLTKTH-----YSPPKFDRGLLGRL 161
Db 422 EF-----ELTIETLKQLOQLKNSQKRSQMASNEPPIDDSFMGMW 463

RESULT 14
UBMUBM
tubulin beta-1 chain - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: JT0275
R;Oppenheimer, D.G.; Haas, N.; Silflow, C.D.; Snustad, D.P.
Gene 63, 87-102, 1988
A;Title: The beta-tubulin gene family of Arabidopsis thaliana: preferential accumulation in roots
A;Reference number: JT0275; MUID:88255862; PMID:3384336
A;Accession: JT0275
A;Molecule type: DNA
A;Residues: 1-447 <OPP>
A;Cross-references: UNIPROT:P12411; GB:M20405; NID:g166921; PIDN:AAA32893.1; PID:g166922
A;Note: the genome of A. thaliana contains a beta-tubulin gene family consisting of at least 10 genes. The transcript of this beta-1 tubulin gene accumulates predominantly in roots
C;Genetics:
A;Introns: 133/1; 223/1
C;Superfamily: tubulin
C;Keywords: microtubule
F:141-147/Region: tubulin/FtsZ GTP/GDP-binding (G-G-G-T-G-[ST]-G) motif

Query Match 7.5%; Score 82.5; DB 1; Length 447;
Best Local Similarity 23.8%; Pred. No. 5.3;
Matches 39; Conservative 21; Mismatches 49; Indels 55; Gaps 8;

QY 12 VGSLLVSGTRGKLPD-----APEFEKDLIIQRLLNMLWV-----IDEC----- 49
Db 148 MGTLLISKIRBEYDPRMMLTFSPSPKV-SDTVVPEYNATLSVHQLVENADECMVLQNE 206

QY 50 -FRDLCVRTGICKGILEPAAIFHLKLPAINDTDHGCLIGFNETS-----LKKL 97
Db 207 ALYDICTFT-----LKUSTPSFGDLNHLISATSGVTCSLRFPQOLNLDRLK 254

QY 98 ADGFFEFEVLFPK-----LTTEFGKSVINVDVNMELTKITLQWD 135

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:12:44 ; Search time 214.063 Seconds
(without alignments)
488.007 Million cell updates/sec

Title: US-10-828-343-2
Perfect score: 1095
Sequence: 1 MCWFKWLSLLVSGT.....GQAVRVLDSIPDTPDVHDK 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	204	2 Q98823	Q98823 human herpe
2	1095	100.0	204	2 Q768K3	Q768K3 human herpe
3	1088	99.4	204	2 Q40918	Q40918 human herpe
4	185	16.9	212	1 IL6 MACFA	P79341 macaca fasc
5	184	16.8	212	2 Q8MKH0	Q8MKH0 saimiri sci
6	183	16.7	212	1 IL6 CERTO	P46650 cercocebus
7	183	16.7	212	1 IL6 HUMAN	P05231 homo sapien
8	182	16.6	209	2 Q9TTH3	Q9TTH3 actus lemur
9	181	16.5	212	1 IL6 MACMU	P51494 macaca mula
10	180.5	16.5	212	1 IL6 PIG	P26893 sus scrofa
11	179	16.3	209	2 Q97540	Q97540 actus nancy
12	177.5	16.2	212	2 Q8M75	Q8M75 sus scrofa
13	173.5	15.8	208	1 IL6 HORSE	Q95181 equus cabal
14	163.5	14.9	208	1 IL6 FELCA	P41683 felis silve
15	162	14.8	211	1 IL6 LAMGL	Q865X6 lama glama
16	160	14.6	214	2 Q8MKES	Q8MKES sus scrofa
17	159.5	14.6	209	1 IL6 PHOVI	Q28819 phoca vitul
18	158	14.4	208	2 Q9XT80	Q9XT80 delphinapte
19	158	14.4	211	2 Q865W7	Q865W7 camelus bac
20	155.5	14.2	205	1 IL6 ORCOR	Q28747 orcinus orc
21	155	14.2	241	2 Q90Y10	Q90Y10 gallus gall
22	154.5	14.1	207	2 Q9MYZ7	Q9MYZ7 canis fami
23	152	13.9	208	1 IL6 CAPHI	Q28319 capra hircu
24	150	13.7	208	1 IL6 SHEEP	P29455 ovis aries
25	148	13.5	211	1 IL6 MOUSE	P08505 mus musculu
26	144.5	13.2	207	1 IL6 CANFA	P41323 canis fami
27	143.5	13.1	208	1 IL6 BOVIN	P26892 bos taurus
28	143	13.1	175	2 Q9TTH4	Q9TTH4 actus nigri
29	139.5	12.7	208	2 Q6V919	Q6V919 bubalus bub
30	138	12.6	207	2 Q9JHH3	Q9JHH3 marmota mon
31	136.5	12.5	207	2 Q28403	Q28403 enhydra lut

32	135	12.3	207	1 IL6 MARMO	O35736 marmota mon
33	134	12.2	211	1 IL6 RAT	P20607 rattus norv
34	132.5	12.1	191	2 Q6QHV3	Q6QHV3 cervus elap
35	132	12.1	160	2 Q97535	Q97535 actus vocif
36	129.5	11.8	210	2 Q9WVQ8	Q9WVQ8 mesocricetu
37	123.5	11.3	212	2 Q912L3	Q912L3 sigmodon hi
38	119.5	10.9	125	1 IL6 MUSVI	P41693 mustela vis
39	116.5	10.6	241	2 Q9MZR1	Q9MZR1 oryctolagus
40	103.5	9.5	108	2 Q9BDL5	Q9BDL5 phocoenoid
41	100.5	9.2	186	2 Q6P257	Q6P257 meriones un
42	96.5	8.8	399	2 Q6N3M6	Q6N3M6 rhodopsedo
43	96	8.8	692	2 Q6DIH6	Q6DIH6 xenopus tro
44	95.5	8.7	690	2 Q6DRG6	Q6DRG6 brachydanio
45	95	8.7	684	1 CPSC_BOVIN	P79101 bos taurus

ALIGNMENTS

RESULT 1
Q98823 ID Q98823 PRELIMINARY; PRT; 204 AA.
AC Q98823;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Interleukin-6 homolog (Fragment).
GN Name=VIL-6;
OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RA Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
RA Friedman-Kien A.-E., Fleckenstein B.;
RT "Human herpesvirus 8 encodes a homologue of interleukin-6";
RL J. Virol. 0:0-0(1996).
DR EMBL; U73655; AAB18244.1; -;
DR PDB; 1IIR; X-ray; B=-;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPRO09079; 4 helix cytokine.
DR InterPro; IPRO03573; IL6_MGF_GCSF.
DR InterPro; IPRO03574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
FT NON_TER 204
SQ SEQUENCE 204 AA; 23408 MW; 1CA7772A0EDC05EB CRC64;

Query Match	100.0%;	Score 1095;	DB 2;	Length 204;
Best Local Similarity	100.0%;	Pred. No. 2.4e-92;	Mismatches 0;	Indels 0;
Matches 204;	Conservative 0;			Gaps 0;
QY	1	MCWFKWLSLLVSGSLVSGTRGKLPDAPFEKDLIIQLRNMLWVIDECFRDLCYRTGIC	60	
Db	1	MCWFKWLSLLVSGSLVSGTRGKLPDAPFEKDLIIQLRNMLWVIDECFRDLCYRTGIC	60	
QY	61	KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKLADGFFEFVLFKPLTFEFGKSVI	120	
Db	61	KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKLADGFFEFVLFKPLTFEFGKSVI	120	
QY	121	NDVVMELLTKTGWDIQEELNKLTKTHYSPKPFDRGLGLGRLOGLYKVMVRFASFYVLSAM	180	
Db	121	NDVVMELLTKTGWDIQEELNKLTKTHYSPKPFDRGLGLGRLOGLYKVMVRFASFYVLSAM	180	
QY	181	EKFAGQAVRVLDSIPDTPDVHDK	204	

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Db      181 EKFAQVAVRVLDSIPDVTDPVHDK 204

RESULT 2
Q76SK3 PRELIMINARY; PRT; 204 AA.
ID Q76SK3;
AC Q76SK3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE ORF K2; functional interleukin-6 vIL-6 homolog (Putative interleukin
DE 6).
OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97184526; PubMed=9032328;
RA Nicholas J., Ruvolo V., Zong J., Ciuffo D., Guo H.G., Reitz M.S.,
RA Hayward G.S.;
RT "A single 13-kilobase divergent locus in the Kaposi sarcoma-associated
RT herpesvirus (human herpesvirus 8) genome contains nine open reading
RT frames that are homologous to or related to cellular proteins.";
RL J. Virol. 71:1963-1974(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97208913; PubMed=9055855;
RA Nicholas J., Ruvolo V.R., Burns W.H., Sandford G., Wan X., Ciuffo D.,
RA Hendrickson S.B., Guo H.G., Hayward G.S., Reitz M.S.;
RT "Kaposi's sarcoma-associated human herpesvirus-8 encodes homologues of
RT macrophage inflammatory protein-1 and interleukin-6.";
RL Nat. Med. 3:287-292(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Sun R., Lin S.-F., Miller G.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094384; PubMed=8939871; DOI=10.1126/science.274.5293.1739;
RA Moore P.S., Boshoff C., Weiss R.A., Chang Y.;
RT "Molecular mimicry of human cytokine and cytokine response pathway
RT genes by KSHV.";
RL Science 274:1739-1744(1996).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97121480; PubMed=8962146; DOI=10.1073/pnas.93.25.14862;
RA Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U67774; AAC61701.1; -
DR EMBL; U71365; AAC34937.1; -
DR EMBL; U75698; AAC57089.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6 MGF GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 204 AA; 23408 MW; 1CA7772A08DC05EB CRC64;

Db      181 EKFAQVAVRVLDSIPDVTDPVHDK 204

Query Match 100.0%; Score 1095; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.4e-92;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCWFKLWSLLVGSLLVSGTRGKLPDAPEFEKDLLIQLRLNMLWVIDECFRDLCYRTGIC 60
Db 1 MCWFKLWSLLVGSLLVSGTRGKLPDAPEFEKDLLIQLRLNMLWVIDECFRDLCYRTGIC 60
QY 61 KGILEPAAIHLKLPAINDDTHCGLIIGNFNETSCILKLAGDGFEEVLKFLTTTFGKSVI 120
Db 61 KGILEPAAIHLKLPAINDDTHCGLIIGNFNETSCILKLAGDGFEEVLKFLTTTFGKSVI 120
QY 121 NVDVWELLTKLGDWIDIOBELNKLTKTHYSPKFDRLGLRLQGLKYWRHPASFVLSAM 180
Db 121 NVDVWELLTKLGDWIDIOBELNKLTKTHYSPKFDRLGLRLQGLKYWRHPASFVLSAM 180
QY 181 EKFAQVAVRVLDSIPDVTDPVHDK 204
Db 181 EKFAQVAVRVLDSIPDVTDPVHDK 204

RESULT 3
O40918 PRELIMINARY; PRT; 204 AA.
ID O40918;
AC O40918;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE ORF K2.
OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97138401; PubMed=8985427;
RA Neipel F., Albrecht J.C., Ensser A., Huang Y.Q., Li J.J.,
RA Friedman-Kien A.E., Fleckenstein B.;
RT "Human herpesvirus 8 encodes a homolog of interleukin-6.";
RL J. Virol. 71:839-842(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97296220; PubMed=9151804;
RA Neipel F., Albrecht J.C., Fleckenstein B.;
RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
RT human herpesvirus 8: determinants of its pathogenicity?";
RL J. Virol. 71:4187-4192(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
RA Friedman-Kien A.E., Fleckenstein B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93872; AAB62676.2; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6 MGF GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 204 AA; 23407 MW; 2F46737820D20B9 CRC64;

Query Match 99.4%; Score 1088; DB 2; Length 204;
Best Local Similarity 99.0%; Pred. No. 1.1e-91;
Matches 202; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCWFKLWSLLVGSLLVSGTRGKLPDAPEFEKDLLIQLRLNMLWVIDECFRDLCYRTGIC 60
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Db 1 MCWFKLSLLVSGTRGKLPDAPPEFEKLIQRLNMLWVIDECFRLCYRTGIC 60
Qy 61 KGILEPAAIFHLKLPAINDTDHCGCLIGFNETSCCLKLADGFFEFVLFKFLTTTFGKSVI 120
Db 61 KGILEPAAIFHLKLPAINDTDHCGCLIGFNETSCCLKLADGFFEFVLFKFLTTTFGKSVI 120
Qy 121 NVDMWELLTKTLGWDIOBELNKLTKTHYSPKFDRLGLLQGLKYVVRHFPASPYVLSAM 180
Db 121 NVDMWELLTKTLGWDIOBELNKLTKTHYSPKFDRLGLLQGLKYVVRHFPASPYVLSAM 180
Qy 181 EKFAQAVRLDSDIPDTPDVHDK 204
Db 181 EKFAQAVRLNLSIPDTPDVHDK 204

RESULT 4
IL6_MACFA STANDARD; PRT; 212 AA.
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name:IL6;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RT Tatsumi M.;
RA "Molecular cloning and expression of cynomolgus monkey interleukin-6."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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CC -----
CC EMBL; AB000554; BAA19148.1; -.
CC HSP; P05231; IL6.
CC InterPro; IPR009079; 4 helix cytokine.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC InterPro; IPR003574; Interleukin_6.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PRINTS; PR00434; INTERLEUKIN_6.
CC ProDom; PD004356; Interleukin_6; 1.
CC SMART; SM00126; IL6; 1.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
CC Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 Interleukin-6.
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBFB0389 CRC64;

Query Match 16.9%; Score 185; DB 1; Length 212;
Best Local Similarity 25.5%; Pred. No. 1e-08;
Matches 50; Conservative 40; Mismatches 98; Indels 8; Gaps 2;

Qy 4 FKLWSLLVLSL-----LVSGTRGKLPDAPPEFEKDLIQLRNMLWV----IDECFRLCY 55
Db 14 FSLGLLVMPAAPAPVTLGDSKEVAAPNQLLTSTERIDKHIVYLDGIALRKEICN 73
Qy 56 RTGICGILEPAAIFHLKLPAINDTDHCGCLIGFNETSCCLKLADGFFEFVLFKFLTTTF 115
Db 74 KSNMCESSKEALAEANNLNLPRMAEKDGCQSGFNEETCLLKITTTGLLEFEVYLEYLNRF 133
Qy 116 GKSVINVDVWELLTKTLGWDIOBELNKLTKTHYSPKFDRLGLLQGLKYVVRHFPASFY 175
Db 134 ESSKEQAGVQVMTSGTLQSLQKAKNLSAIAITPDPAATNLSLTKQAQDQWVTHL 193
Qy 176 VLSAMEKFAQAVRVL 191

Best Local Similarity 26.3%; Pred. No. 8.2e-09;
Matches 51; Conservative 36; Mismatches 93; Indels 14; Gaps 2;

Qy 12 VGSLLVSGTRGKLPDAP-BFEKDL-----LIQRLNMLWVIDECFRLCYRT 57
Db 16 LGILLVLPAAFPAPVLPGEDSKDVAAPHOSQPLTSSEKIDKHIRIYLDGIALRKETCNRS 75
Qy 58 GICKGILEPAAIFHLKLPAINDTDHCGCLIGFNETSCCLKLADGFFEFVLFKFLTTTFGK 117
Db 76 NMCSSKEALAEANNLNLPRMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYLNRFES 135
Qy 118 SVINVDVWELLTKTLGWDIOBELNKLTKTHYSPKFDRLGLLQGLKYVVRHFPASFYVL 177
Db 136 SEQARAVQVMTSGTLQSLQKAKNLSAIAITPDPAATNLSLTKQAQDQWVTHL 195
Qy 178 SAMEKFAQAVRVL 191
Db 196 RSPKFEQLQSSRAL 209

RESULT 5
Q8MKH0 PRELIMINARY; PRT; 212 AA.
AC Q8MKH0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin-6.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RT MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-Y;
RA Heraud J.M., Lavergne A., Kazanji M.;
RA "Molecular cloning, characterization, and quantification of squirrel monkey (Saimiri sciureus) Th1 and Th2 cytokines.";
RL Immunogenetics 54:20-29(2002).
DR EMBL; AF294757; AAK92044.1; -.
DR HSP; P05231; IL6.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR SEQUENCE 212 AA; 23581 MW; FF22CBFA93245479 CRC64;

Query Match 16.8%; Score 184; DB 2; Length 212;
Best Local Similarity 25.5%; Pred. No. 1e-08;
Matches 50; Conservative 40; Mismatches 98; Indels 8; Gaps 2;

Qy 4 FKLWSLLVLSL-----LVSGTRGKLPDAPPEFEKDLIQLRNMLWV----IDECFRLCY 55
Db 14 FSLGLLVMPAAPAPVTLGDSKEVAAPNQLLTSTERIDKHIVYLDGIALRKEICN 73
Qy 56 RTGICGILEPAAIFHLKLPAINDTDHCGCLIGFNETSCCLKLADGFFEFVLFKFLTTTF 115
Db 74 KSNMCESSKEALAEANNLNLPRMAEKDGCQSGFNEETCLLKITTTGLLEFEVYLEYLNRF 133
Qy 116 GKSVINVDVWELLTKTLGWDIOBELNKLTKTHYSPKFDRLGLLQGLKYVVRHFPASFY 175
Db 134 ESSKEQAGVQVMTSGTLQSLQKAKNLSAIAITPDPAATNLSLTKQAQDQWVTHL 193
Qy 176 VLSAMEKFAQAVRVL 191

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Db 16 LGLLLVLPAAFPAPVPBGSDSKDAVAPHRQPLTSSRTIDKQIRYILDGISALRKETCNKS 75
QY 58 GICKGILEPAAIFHLKLPAINDTDHGILGFNETSCILKKLADGFFEFVLFKFLTTERGK 117
Db 76 NNCSSKEALAEENLNLPKVAEKDGFQSGFNEETCLVKIITGLLEFEVYLEYLNQRPFS 135
QY 118 SVINVDVMELLTKTGLWDIQBELNKLTKTHYSPKFDRLGLRLOGLKYNVVRHFAFVYL 177
Db 136 SEEQARAVQMSKVLIOFLQKAKNLDAITTDPPTNASLLTKLQANQWLQDMTHLLIL 195
QY 178 SAMEKFAQAVRVL 191
Db 196 RSFKEFLQSSLRAL 209

RESULT 8

Q9TTH3 PRELIMINARY; PRT; 209 AA.
AC Q9TTH3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAY-2000 (Tremblrel. 26, Last annotation update)
GN Name=IL-6;
OS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=43147;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murillo L.A., Patarroyo M.E.;
RT "Identification, cloning, and sequencing of different cytokine genes
in four species of owl monkey."
RL Immunogenetics 54:645-653(2002).
DR EMBL; AF097323; AAF21298.1; -.
DR HSP; P05231; 1ALU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4.helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFPMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
FT NON_TER 209 209
SQ SEQUENCE 209 AA; 23115 NW; AOA3DFAA4BF560CC CRC64;

Query Match 16.6%; Score 182; DB 2; Length 209;
Best Local Similarity 26.5%; Pred. No. 1.5e-08;
Matches 41; Conservative 36; Mismatches 78; Indels 0; Gaps 0;

QY 37 QRLNWLWIDCFRDLVCRVTGICKGILEPAAIFHLKLPAINDTDHGILGFNETSCILKK 96
Db 55 KHIRILEGISALRKEICDKSNWCSSKEALAEENLNLPKVAEKDGFQSGFNEETCLVK 114
QY 97 LADGFFEFVLFKFLTTEFGKSVINVDVMELLTKTGLWDIQBELNKLTKTHYSPKFDGR 156
Db 115 IITGLLEFEVYLEYLNQRPFSKEQAGAVQMSKGLQSLQKAKNLSAIAITPDATNAS 174
QY 157 ILGRLOGLKYNVVRHFAFVYLSAMEKFAQAVRVL 191
Db 175 LLMKLOAQDQWLQGVVTHILRSFKEFLQSSLRAL 209

RESULT 9

IL6_MACMU
ID IL6_MACMU STANDARD; PRT; 212 AA.
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAC 2;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger P.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation, in
hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.

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or send an email to license@isb-sib.ch).

DR EMBL; L26028; AAA99978.1; -.
DR HSP; P05231; 1ALU.
DR InterPro; IPR009079; 4.helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFPMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 By similarity.
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 212 AA; 23728 MW; 4130DFE0CF0BCCAD CRC64;

Query Match 16.5%; Score 181; DB 1; Length 212;
Best Local Similarity 25.5%; Pred. No. 1.9e-08;
Matches 50; Conservative 40; Mismatches 98; Indels 8; Gaps 2;

QY 4 PKLWSLLVGSU----LVSGTRGKLPDAPEF-----KDLLIQRLNWLWIDCFRDLCY 55
Db 14 FSLGULLLVPAFPAPVLPDGSKNVAAPHQSPLTSSERIDKHRYIIDGHSALRKTCN 73
QY 56 RTGICKGILEPAAIFHLKLPAINDTDHGILGFNETSCILKKLADGFFEFVLFKFLTTEF 115
Db 74 RSNWCSSKEALAEENLNLPKVAEKDGFQSGFNEETCLVKIITGLLEFEVYLEYLNQRF 133
QY 116 GKSVINVDVMELLTKTGLWDIQBELNKLTKTHYSPKFDRLGLRLOGLKYNVVRHFAF 175
Db 134 ESSSEQARAVQMSKVLIOFLQKAKNLDAITTDPPTNASLLTKLQANQWLQDMTHL 193

QY 176 VLSMEKFAQAVRVL 191
 Db 194 ILRSFKFQSNLRAL 209

RESULT 10
 IL6_PIG
 ID IL6_PIG STANDARD; PRT; 212 AA.
 AC P26893; Q95KN6;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91339547; PubMed=1873476; DOI=10.1016/1043-4666(91)90494-X;
 RA Richards C., Saklatvala J.;
 RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
 expression of mRNA in synovial fibroblasts in vitro.";
 RL Cytokine 3:269-276(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92360284; PubMed=1497880;
 RA Mathialagan N., Bixby J.A., Roberts M.R.;
 RT "Expression of interleukin-6 in porcine, ovine, and bovine
 preimplantation conceptuses.";
 RL Mol. Reprod. Dev. 32:324-330(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Landrace x Meishan; TISSUE=Blood;
 RA Liu S., Meng M., Gao R.;
 RT "Cloning and expression of interleukin 6 gene from Landrace x Meishan
 hybrid swine.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 functions: it plays an essential role in the final differentiation
 of B-cells into Ig-secreting cells, it induces myeloma and
 plasmacytoma growth, it induces nerve cells differentiation, in
 hepatocytes it induces acute phase reactants.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: Belongs to the IL-6 superfamily.
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 or send an email to license@isb-sib.ch).
 CC ENBL; M86722; AAC37333.1; -.
 CC ENBL; M80258; AAC27127.1; -.
 CC ENBL; AF309651; AAC27730.1; -.
 CC PIR; I46590; I46590.
 CC PIR; I46621; I46621.
 CC HSP; P05231; IALU.
 CC InterPro; IPR009079; 4 helix cytokine.
 CC InterPro; IPR003573; IL6_MGF_GCSF.
 CC InterPro; IPR003574; Interleukin_6.
 CC Pfam; PF00489; IL6; 1.
 CC PRINTS; PR00433; IL6GCSFMGF.
 CC PRINTS; PR00434; INTERLEUKIN_6.
 CC ProDom; PD004356; Interleukin_6; 1.
 CC SMART; SM00126; IL6; 1.
 CC PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 By similarity.
 FT CHAIN 30 212 Interleukin-6.

FT DISULFID 72 78 By similarity.
 FT DISULFID 101 111 By similarity.
 FT CONFLICT E -> G (in Ref. 1).
 SQ SEQUENCE 212 AA; 23952 MW; 1E736FB230B4FC5D CRC64;

Query Match 16.5%; Score 180.5; DB 1; Length 212;
 Best Local Similarity 23.9%; Pred. No. 2.1e-08;
 Matches 47; Conservative 46; Mismatches 87; Indels 17; Gaps 2;

QY 12 VGSLLVSGTRGKLPDAPPEP-----KDLIQLRNWMLWIDECFRDLVCRT 57
 Db 16 LGILLWATAFPPTPERLEEDAKGATSDKMLFTSPDKTEELIKYILGKISAMRKEMCKY 75
 QY 58 GICKGILEPAAIFHLKLPAINDTDHGCLIGNETSCIKLADGFEFEVLFKFLTTBFGK 117
 Db 76 EKCEKSEKVLAEENNLNPKMAEKDGCFCQSGFNQETCLMRITTTGLVFQIVLDYLQKEYS 135
 QY 118 SVINVDVMELLTKLGDWIDQBELNKLTKTHYSPKFDRLGLRLQGLKYLWYRHPASPYVL 177
 Db 136 NKGNEVAQVISTKALITQLRQKGNPKDKATTPNPTTNAAGLLDKLQSQNEWMKNTKIIL 195
 QY 178 SAME---KPAQOAVRVL 191
 Db 196 RSLIEDFLQFSIRIRIM 212

RESULT 11
 QY7540 PRELIMINARY; PRT; 209 AA.
 ID QY7540;
 AC QY7540;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-6 (Fragment).
 GN Name=IL-6;
 OS Aotus nancymae (Ma's night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=37293;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=223541394; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
 RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
 RA Murillo L.A., Patarroyo M.E.;
 RT "Identification, cloning, and sequencing of different cytokine genes
 in four species of owl monkey.";
 RL Immunogenetics 54:645-653(2002).
 DR ENBL; AF014510; AAD01536.1; -.
 DR HSP; P05231; IALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 FT NON_TER 1 1
 FT NON_TER 209 209
 SQ SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match 16.3%; Score 179; DB 2; Length 209;
 Best Local Similarity 26.5%; Pred. No. 2.9e-08;
 Matches 41; Conservative 34; Mismatches 80; Indels 0; Gaps 0;

QY 37 QRLNWMWIDECFRDLVCRTGICKGILPAAIFHLKLPAINDTDHGCLIGNETSCIKK 96
 Db 55 KHIRYLDGISALRKETCKNSNCESSKEALAENNLNPKMAEKDGCFCQSGFNTEETCLVK 114

```
QY 97 LADGFEFVRLFKLTTRTFKGVINVDVWMLLTKTLGWDIOBELNKLTKTHYSPKFDRG 156
Db 115 IITGLLEFVEYIYQNRFESEBQARVOMTKVLIQFLQKKAKNLDIAITTPDPTTNAS 174
QY 157 LLGRQLGKYVVRHFASFYVLSAMEKFAQAVRVL 191
Db 175 LUTLQAQNWQLQDMTHLILASFKFLOSSLRAL 209

RESULT 12
Q8MJ75 PRELIMINARY; PRT; 212 AA.
AC Q8MJ75;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IL-6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee D., Yoo H., Choi I.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF518322; AMW4938.1; -.
DR HSP; P05231; IALU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 212 AA; 23881 MW; 1F540E7030BCFD77 CRC64;

Query Match 16.2%; Score 177.5; DB 2; Length 212;
Best Local Similarity 23.9%; Pred. No. 48-08;
Matches 48; Conservative 48; Mismatches 80; Indels 25; Gaps 4;

QY 12 VGSLLVSGTR-----GKLPD-----APEFEKDLIIQLRLNMLWLVIDSCFRDL 53
Db 16 LGLLLVMATAFPTPGLEDAKGDATSKMLFTSPDKTEEL-----IKYLKGKISAMREEM 71
QY 54 CVRTGICKGILEPAAIFHLKLPAINDTHCGILIGNFNETSCLKLADGPFEPFVLPKFLTT 113
Db 72 CEKYCKENSKSVLAENNLNLPMAEKDGCQFSGFNQETCLMRITTLGLVFEQIYLDLYLQK 131
QY 114 EFGKSVINVDVWMLLTKTLGWDIOBELNKLTKTHYSPKFDGILGRLOGLKYVVRHFAS 173
Db 132 EYESKNGVNEAVQISTKALIQTLRQKGNPKATPTNPTNAGLLDKLQSQNEWMKNTKI 191
QY 174 FYVLSAME---KFAGQAVRVL 191
Db 192 IILRSLEDPLQFSLRAIRIM 212

RESULT 13
IL6 HORSE
ID IL6 HORSE STANDARD; PRT; 208 AA.
AC Q95T81; O19007; O46568;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
```

```
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Swiderski C.E., Sobol G., Lunn D.P., Horchov D.W.;
RL "Molecular cloning, sequencing, and expression of equine interleukin-6.";
RT Vet. Immunol. Immunopathol. 77:213-220(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
RL "Molecular cloning of equine interleukin-6.";
RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lai A.C.K.;
RL "Cloning and expression of equine interleukin-6.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
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DR EMBL; U64794; AAB87703.1; -.
DR EMBL; AF005227; AAB62246.1; -.
DR EMBL; AF041975; AAC04574.1; -.
DR PIR; T09216; T09216.
DR HSP; P05231; IALU.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 208 Interleukin-6.
FT DISULFD 69 75 By similarity.
FT DISULFD 98 108 By similarity.
FT CARBOHYD 71 71 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 184 184 N-linked (GLCNAC...) (Potential).
FT CONFLICT 4 5 LS -> FF (in Ref. 1).
FT CONFLICT 8 8 T -> A (in Ref. 3).
FT CONFLICT 137 137 I -> V (in Ref. 2).
FT CONFLICT 205 205 V -> I (in Ref. 3).
SQ SEQUENCE 208 AA; 23325 MW; A62F4C234056BF66 CRC64;

Query Match 15.8%; Score 173.5; DB 1; Length 208;
Best Local Similarity 26.0%; Pred. No. 9.1e-08;
Matches 51; Conservative 37; Mismatches 89; Indels 19; Gaps 5;

QY 12 VGSLLVSGTRKLP-----DAPEFEKDLII-----QLRLNMLWLVIDSCFRDLCYRTGIC 60
Db 16 LGLLLVMATAFPTPLGLEDGDETTNGPLLTADTKQHKIKISALKNEMCNFNFSKC 75
QY 61 KGILEPAAIFHLKLPAINDTHCGILIGNFNETSCLKLADGPFEPFVLPKFLTTTFEGKSVI 120
```


Db 76 ENSKEVLAENNLNPKWAEDKCCQSGFNQSTGLSEFQIYLYEQNEFKGEKE 135
 Qy 121 NVDVWELLTKTGLWDIOBELNKLTKTHYS--PPKFDRLGLRLQGLKYVVRHFPASFVYLS 178
 Db 136 NIKTMQISTKVL---VQILQKMKNPVPTPDPTAKSSLLAKLHNSQENWLNKNTTHILIR 192
 Qy 179 AME---KFGAQVRL 191
 Db 193 SLEDFLQFSLRAVRIM 208

RESULT 14
 IL6_FELCA STANDARD; PRT; 208 AA.
 AC P41683;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94162386; PubMed=8117820;
 RA Ohashi T., Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H.,
 RA Hasegawa A.;
 RT "Molecular cloning of feline interleukin-6 cDNA."
 RL J. Vet. Med. Sci. 55:941-944 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=94052249; PubMed=8234373;
 RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
 RT "Molecular cloning and characterization of a cDNA encoding feline
 interleukin-6."
 RL Proc. Soc. Exp. Biol. Med. 204:301-305 (1993).
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 functions: it plays an essential role in the final differentiation
 of B-cells into Ig-secreting cells, it induces myeloma and
 plasmacytoma growth, it induces nerve cells differentiation, in
 hepatocytes it induces acute phase reactants.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.

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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; L16914; AAA16620.1; -;
 CC DR EMBL; D13227; BAA02507.1; -;
 CC DR PIR; I46084; I46084.
 CC DR HSP; P05231; IL6.
 CC DR InterPro; IPR009079; 4 helix cytokine.
 CC DR InterPro; IPR003573; IL6_MGF_GCSP.
 CC DR InterPro; IPR003574; Interleukin_6.
 CC DR Pfam; PF00489; IL6; 1.
 CC DR PRINTS; PR00433; IL6GCSPMGF.
 CC DR PRINTS; PR00434; INTERLEUKIN6.
 CC DR SMART; SM00126; IL6; 1.
 CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 208 Interleukin-6.
 FT DISULFID 68 74 By similarity.

FT DISULFID 97 107 By similarity.
 FT CONFLICT 2 2 T -> N (in Ref. 2).
 FT CONFLICT 45 45 S -> P (in Ref. 2).
 FT CONFLICT 133 133 E -> K (in Ref. 2).
 FT CONFLICT 173 187 AKLOSQEWLRHTTI -> LSCSHRRVAAEHNH (in
 Ref. 2).
 FT CONFLICT 200 201 FS -> LR (in Ref. 2).
 SQ SEQUENCE 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;

Query Match 14.9%; Score 163.5; DB 1; Length 208;
 Best Local Similarity 26.8%; Pred. No. 7.5e-07;
 Matches 55; Conservative 39; Mismatches 84; Indels 27; Gaps 7;

Qy 4 FKLWSLLV-----GSLVSGTRGKLPDAPFEKDLIQLRLNMLWVDECFRDLCYR 56
 Db 14 FSLGLLVVATAPPTPLGGDATSNRLPLT---SADKMEELIKYILGKISALKKEMCDN 70
 Qy 57 TGICKGILEPAAIFHLKLPAINDTDHGGLIGFNETSCLKLADGPFEPFVFLFELTTEP- 115
 Db 71 YNKCEDSKALAEANLNLPKLAEGKQCGSQSGFNQETCLTRITTTGLOBFQIYLFQDKYE 130
 Qy 116 ----GKSV-INVDVMEELTKTGLWDIOBELNKLTKTHYSPPKFDRLGLRLQGLKYVVR 169
 Db 131 GDEENAKSVTSTNVLLQMLKRGKN-QDEVT-----IPVPTVEVLQALQSQEWEWR 183
 Qy 170 HFASFYVLSAME---KFGAQVRL 191
 Db 184 HTTILTLRLLEDLFQFSLRAVRIM 208

RESULT 15
 IL6_LAMGL STANDARD; PRT; 211 AA.
 AC Q865X6;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Lama glama (Llama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OX NCBI_TaxID=9844;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Raadan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,
 RA Onuma M.;
 RT "Cloning and sequence analysis of cytokine cDNAs of llama and camel."
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 functions: it plays an essential role in the final differentiation
 of B-cells into Ig-secreting cells, it induces myeloma and
 plasmacytoma growth, it induces nerve cells differentiation, in
 hepatocytes it induces acute phase reactants (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.

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 CC
 CC EMBL; AB107647; BAC75384.1; -;
 CC DR HSP; P05231; IL6.
 CC DR InterPro; IPR009079; 4 helix cytokine.
 CC DR InterPro; IPR003573; IL6_MGF_GCSP.
 CC DR InterPro; IPR003574; Interleukin_6.
 CC DR Pfam; PF00489; IL6; 1.
 CC DR PRINTS; PR00433; IL6GCSPMGF.
 CC DR PRINTS; PR00434; INTERLEUKIN6.

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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:09:54 ; Search time 21.0448 Seconds
(without alignments)
349.180 Million cell updates/sec

Title: US-10-828-343-2_COPY_87_105
Perfect score: 103
Sequence: 1 GFNETSCLKLAGFFFE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	19	2 AAW23945	Aaw23945 Human her
2	103	100.0	185	2 AAW95015	Aaw95015 Kaposi's
3	103	100.0	204	2 AAW40103	Aaw40103 Human her
4	103	100.0	204	2 AAW23944	Aaw23944 Human her
5	103	100.0	204	2 AAW74570	Aaw74570 Kaposi sa
6	61	59.2	118	7 ADH76487	Adh76487 Interleuk
7	61	59.2	125	7 ADH76486	Adh76486 Interleuk
8	61	59.2	148	4 AAU02910	Aau02910 Angiotens
9	61	59.2	157	7 ADF17513	Adf17513 MB-2 amin
10	61	59.2	162	2 AAR77391	Aar77391 Human mut
11	61	59.2	162	2 AAW00131	Aaw00131 Human int
12	61	59.2	163	2 AAW00132	Aaw00132 Human int
13	61	59.2	166	6 ABU62834	Abu62834 Human int
14	61	59.2	166	6 ABU62837	Abu62837 Monkey in
15	61	59.2	166	7 ADC20004	Adc20004 Rhesus mo
16	61	59.2	166	7 ADC20001	Adc20001 Human int
17	61	59.2	167	7 ADF17512	Adf17512 MB-1 amin
18	61	59.2	167	2 AAR77649	Aar77649 Human int
19	61	59.2	169	2 AAR77387	Aar77387 Human IL-
20	61	59.2	174	2 AAR75342	Aar75342 Hybrid hu
21	61	59.2	176	2 AAR75341	Aar75341 Hybrid hu
22	61	59.2	177	2 AAR77388	Aar77388 Human IL-
23	61	59.2	179	2 AAR75334	Aar75334 Human int
24	61	59.2	182	6 ABP72700	Abp72700 Human int
25	61	59.2	183	2 AAR60125	Aar60125 Human int

26	61	59.2	183	8 ADL89570	Adl89570 Human mod
27	61	59.2	183	8 ADL89594	Adl89594 Human mod
28	61	59.2	183	8 ADL89599	Adl89599 Human mod
29	61	59.2	183	8 ADL89602	Adl89602 Human mod
30	61	59.2	183	8 ADL89563	Adl89563 Human mod
31	61	59.2	183	8 ADL89567	Adl89567 Human mod
32	61	59.2	183	8 ADL89597	Adl89597 Human mod
33	61	59.2	183	8 ADL89564	Adl89564 Human mod
34	61	59.2	183	8 ADL89571	Adl89571 Human mod
35	61	59.2	183	8 ADL89580	Adl89580 Human mod
36	61	59.2	183	8 ADL89587	Adl89587 Human mod
37	61	59.2	183	8 ADL89593	Adl89593 Human mod
38	61	59.2	183	8 ADL89585	Adl89585 Human mod
39	61	59.2	183	8 ADL89590	Adl89590 Human mod
40	61	59.2	183	8 ADL89603	Adl89603 Human mod
41	61	59.2	183	8 ADL89604	Adl89604 Human mod
42	61	59.2	183	8 ADL89562	Adl89562 Human mod
43	61	59.2	183	8 ADL89586	Adl89586 Human mod
44	61	59.2	183	8 ADL89596	Adl89596 Human mod
45	61	59.2	183	8 ADL89605	Adl89605 Human mod

ALIGNMENTS

RESULT 1
AAW23945
ID AAW23945 standard; protein; 19 AA.
AC AAW23945;
XX
DT 01-JUL-1998 (first entry)
XX
DE Human herpesvirus 8 interleukin-6 fragment.
XX
KW interleukin-6; IL-6; human herpesvirus 8; HHV8; shotgun-cloning;
KW Antibodies; diagnosis; treatment.
XX
OS Human herpesvirus 8.
XX
PN WO9803657-A1.
XX
PD 29-JAN-1998.
XX
PF 19-JUL-1996; 96WO-EP003199.
XX
PR 19-JUL-1996; 96WO-EP003199.
XX
PA (BEHW) BEHRING DIAGNOSTICS GMBH.
PA (UYN) UNIV NEW YORK STATE.
PI Fleckenstein B, Albrecht J, Neipel F, Friedman-Kien A, Huang Y;
XX WPI; 1998-120781/11.
XX
PT Viral interleukin-6 produced recombinantly from human herpes virus 8 DNA
PT - and related nucleic acid and antibodies, used for diagnosis and
PT treatment of herpes 8 infection or related diseases, e.g. Kaposi sarcoma.
XX
PS Claim 4; Page 8; 19pp; English.
XX
CC The interleukin-6 (IL-6) fragment and protein AAW23944 can be used to
CC detect antibodies and antibodies can be used to detect IL-6. This can be
CC used for the diagnosis of HHV8 infection or associated diseases such as
CC Kaposi sarcoma or kidney cell carcinoma. Antibodies, proteins and the
CC gene sequence can all be used in the treatment of infections and diseases
CC as mentioned above
SQ Sequence 19 AA;

Query Match 100.0%; Score 103; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GNETSCLKKLADGFFFE 19
DB 1 GNETSCLKKLADGFFFE 19

RESULT 2
AAW95015
ID AAW95015 standard; peptide; 185 AA.
AC AAW95015;
XX 27-AUG-2003 (revised)
XX 21-MAY-1999 (first entry)
XX Kaposi's sarcoma herpes virus interleukin-6 (IL-6) polypeptide.
DE Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;
XX inflammatory condition; drug screening; human; IL-6.
XX Human herpesvirus 8.
OS WO9905280-A1.
XX 04-FEB-1999.
XX 24-JUL-1998; 98WO-US015423.
XX 25-JUL-1997; 97US-00900905.
XX (SCHE ) SCHERING CORP.
XX Bazan JF;
XX WPI; 1999-142935/12.
XX Newly isolated or recombinant polynucleotide encoding mammalian cytokine
XX interleukin-B30 (IL-B30), including fragments - useful for regulating
XX activation, development, differentiation and function of various cell
XX types, and for diagnosing and treating conditions associated with IL-B30.
XX Disclosure; Page 11-12; 83pp; English.
XX This invention relates to mammalian cytokine interleukin-B30 (IL-B30)
XX polypeptides. Host cells containing a vector comprising the IL-B30
XX nucleic acids are used for the recombinant production of the proteins.
XX The polynucleotides are useful for diagnosis of IL-B30 mediated
XX conditions, and forensic science (e.g. to distinguish rodent from human,
XX or as a marker to distinguish between different cells exhibiting
XX differential expression or modification patterns). The IL-B30 (including
XX fragments), together with antibodies that bind to IL-B30 are useful for
XX teaching purposes. They are also used for treating conditions associated
XX with abnormal physiology or development, including inflammatory
XX conditions. The polypeptide cytokine should mediate cytokine synthesis
XX and proliferation in cells. IL-B30 is useful for drug screening to
XX identify compounds having binding affinity to IL-B30. The present
XX sequence represents a Kaposi's sarcoma herpes virus IL-6. (Updated on 27
XX -AUG-2003 to correct OS field.)
XX Sequence 185 AA;

Query Match 100.0%; Score 103; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGFFFE 19
DB 68 GNETSCLKKLADGFFFE 86

RESULT 3
AAW40103
ID AAW40103 standard; protein; 204 AA.

```

```

XX AC AAW40103;
XX 27-AUG-2003 (revised)
XX 15-JUL-1998 (first entry)
XX Human herpesvirus 8 (HHV-8) interleukin-6.
XX DL-B; thymidylate synthase; dihydrofolate reductase; primer; HHV-8;
XX Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein;
XX Kaposi's sarcoma; beta-chemokine-like; amplification; PCR; vIL-6.
XX Human herpesvirus 8.
XX WO9804284-A1.
XX 05-FEB-1998.
XX 24-JUL-1997; 97WO-US012931.
XX 25-JUL-1996; 96US-0022591P.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Hayward GS, Nicholas J, Reitz MR, Hardwick JM;
XX WPI; 1998-130422/12.
XX New human herpes virus gene region containing 8 open reading frames -
XX useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based large
XX cell lymphoma.
XX Claim 1; Page 59-60; 84pp; English.
XX The sequence represents a novel human herpesvirus 8 (HHV-8) interleukin-
XX 6. The invention claims for novel genes, which includes the viral
XX interleukin-6 gene, found at the divergent DL-B locus. HHV-8 divergent
XX locus DL-B lies between open reading frames 11 and 17. Sequencing of the
XX HHV-8 divergent locus DL-B revealed the presence of nine viral ORFs with
XX gene products related to cellular proteins. These proteins include the
XX thymidylate synthase (TS, AAW40100), dihydrofolate reductase (DHFR, see
XX AAW40101), Bcl-2 homologue (AAW40102), IE-1A (AAW40107), IE-1B (AAW40108)
XX and four cytokines which include viral interleukin-6 (vIL-6), viral
XX macrophage inhibitory protein (vMIP)-1A (AAW40104) and -1B (AAW40105) and
XX beta-chemokine-like (BCK, AAW40106) protein. The invention claims the
XX mentioned proteins and a polynucleotide containing HHV-8 genes encoding
XX one or more of these proteins. The invention also claims that the
XX polynucleotide and the proteins may be used directly or indirectly, e.g.
XX using antibodies to the proteins, to diagnose an HHV-8 associated
XX disease, e.g. Kaposi's sarcoma, Castleman's disease, multiple myeloma and
XX body cavity based large cell lymphoma (BCBL). The proteins have also been
XX claimed to be useful in screening compounds for drugs to treat HHV-8
XX diseases. (Updated on 27-AUG-2003 to correct OS field.)
XX Sequence 204 AA;

Query Match 100.0%; Score 103; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGFFFE 19
DB 87 GNETSCLKKLADGFFFE 105

RESULT 4
AAW23944
ID AAW23944 standard; protein; 204 AA.
XX AAW23944;
XX 30-JUN-1998 (first entry)

```

DE Human herpesvirus 8 interleukin-6.
 XX interleukin-6; IL-6; human herpesvirus 8; HHV8; shotgun-cloning;
 KW antibody; diagnosis; treatment.
 XX Human herpesvirus 8.
 OS WO9803657-A1.
 PN 29-JAN-1998.
 XX 19-JUL-1996; 96WO-EP003199.
 XX 19-JUL-1996; 96WO-EP003199.
 XX (BEHW) BEHRING DIAGNOSTICS GMBH.
 PA (UYNV) UNIV NEW YORK STATE.
 XX Fleckenstein B, Albrecht J, Neipel F, Friedman-Kien A, Huang Y;
 PI WPI; 1998-120781/11.
 XX Viral interleukin-6 produced recombinantly from human herpes virus 8 DNA
 PT - and related nucleic acid and antibodies, used for diagnosis and
 PT treatment of herpes 8 infection or related diseases, e.g. Kaposi sarcoma.
 XX Claim 2; Fig 2; 19pp; English.
 PS
 CC The interleukin-6 (IL-6) and protein AAW23945 derived from the sequence
 CC can be used to detect antibodies and antibodies can be used to detect IL-
 CC 6. This can be used for the diagnosis of HHV8 infection or associated
 CC diseases such as Kaposi sarcoma or kidney cell carcinoma. Antibodies,
 CC proteins and the gene sequence can all be used in the treatment of
 CC infections and diseases as mentioned above
 XX
 XX Sequence 204 AA;
 *SQ
 Query Match 100.0%; Score 103; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFNETSCLKKLADGFFFE 19
 DB 87 GFNETSCLKKLADGFFFE 105
 RESULT 5
 AAW74570
 ID AAW74570 standard; protein; 204 AA.
 XX AAW74570;
 AC
 XX 04-DEC-1998 (first entry)
 DT
 XX Kaposi sarcoma herpes-like virus/interleukin-6.
 DE
 XX Kaposi sarcoma herpes-like virus/interleukin-6; PCR; primer;
 KW antiviral agent; multiple myeloma; vaccine; rheumatoid arthritis;
 KW monoclonal gammopathy of undetermined significance; MGUS; malignant;
 KW interleukin-6; Alzheimer's disease; multiple sclerosis; scleroderma;
 KW systemic lupus erythematosus; amplification.
 XX
 XX Synthetic.
 OS
 XX WO9835684-A2.
 PN 20-AUG-1998.
 XX 12-FEB-1998; 98WO-US002820.
 XX 14-FEB-1997; 97US-00800710.
 PR 11-NOV-1997; 97US-00967504.
 XX

PA (BERE/) BERENSON J R.
 PA (RETT/) RETTIG M B.
 PA (VESC/) VESCIO R A.
 XX Berenson JR, Rettig MB, Vescio RA;
 PI WPI; 1998-480765/41.
 XX N-PSDB; AAV54070.
 DR Treatment of multiple myeloma and monoclonal myopathy with antiviral
 PT agent - active against Kaposi sarcoma virus, or with inhibitory nucleic
 PT acid or antibody against this virus.
 XX Disclosure; Fig 5B; 137pp; English.
 PS
 XX This is the amino acid sequence of the Kaposi sarcoma herpes-like
 CC virus/interleukin-6, used in the method of the invention. In this method,
 CC an antiviral agent effective against Kaposi sarcoma herpes-like virus
 CC (KSHV), is used to prevent progression of MGUS to multiple myeloma or
 CC related malignancy. KHSV- and/or interleukin-6 related disorders such as
 CC specifically Alzheimer's disease, multiple sclerosis, rheumatoid
 CC arthritis, systemic lupus erythematosus, scleroderma and malignancies of
 CC kidney or head/neck. The vaccines (comprising a KHSV-specific immunogen)
 CC is used to produce a therapeutic and/or prophylactic response
 XX
 XX Sequence 204 AA;
 Query Match 100.0%; Score 103; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFNETSCLKKLADGFFFE 19
 DB 87 GFNETSCLKKLADGFFFE 105
 RESULT 6
 ADH76487
 ID ADH76487 standard; protein; 118 AA.
 XX ADH76487;
 AC
 XX 22-APR-2004 (first entry)
 DT
 XX Interleukin-6 inhibiting human PAC3 protein, SEQ ID No 4.
 DE
 XX PAC3; interleukin-6; IL-6; inhibitor; IL-6-inhibitory; lymphoma;
 KW leukaemia; myeloma; carcinoma; sarcoma; chronic inflammation; bacterial;
 KW viral infection; osteolysis; degenerative disease;
 KW immunological disorder; transgenic animal; human.
 XX
 XX Homo sapiens.
 OS
 XX FR2833011-A1.
 PN 06-JUN-2003.
 XX 04-DEC-2001; 2001FR-00015623.
 PF
 XX 04-DEC-2001; 2001FR-00015623.
 PR
 XX (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
 PA (BERA-) CENT BERARD LEON.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (HOSP-) HOSPICES CIVILS LYON.
 XX
 XX Blay JY, Alberti L;
 PI WPI; 2003-471810/45.
 DR
 XX New protein PAC3, useful for treating cancers, is an inhibitor of
 PT interleukin-6, also related peptides, nucleic acid, antisense
 PT oligonucleotides and transformed cells.

XX	Claim 3; SEQ ID NO 4; 39pp; French.	PT	interleukin-6, also related peptides, nucleic acid, antisense oligonucleotides and transformed cells.
XX		PS	Claim 1; SEQ ID NO 3; 39pp; French.
CC	The invention relates to a novel protein, PAC3, which inhibits interleukin-6 (IL-6) and has a 125 amino acid sequence, given in the specification. The invention further relates to: peptide fragments of PAC3 with IL-6-inhibitory activity, formed by addition, suppression and/or replacement of one or more amino acids; a nucleic acid that encodes PAC3 or the fragments of the nucleic acid; antisense oligonucleotides that block transcription or translation of PAC3 or its fragments, able to hybridize to the PAC3 coding nucleic acid; a transgenic, non-human animal that expresses a transgene for PAC3 or its fragments; an expression vector containing PAC3 coding nucleic acid and expression elements; and microorganisms or host cells transformed with the vector containing the PAC3 coding nucleic acid and expression elements. The PAC3 protein, and its active fragments, are used to treat lymphoma, leukaemia, myeloma, carcinoma and sarcoma, other conditions induced by, or associated with, overexpression of interleukin-6, e.g. chronic inflammation, bacterial or viral infections, osteolysis in degenerative diseases and immunological disorders. The nucleic acid that encodes PAC3 can be used for recombinant production of the protein and to prepare transgenic animals, useful as models for studying, in vivo, perturbations of the cell cycle and proliferation caused by abnormal or excessive expression of the PAC3 coding nucleic acid, or its truncated or mutated forms. This sequence represents a human PAC3 protein of the invention.	CC	The invention relates to a novel protein, PAC3, which inhibits interleukin-6 (IL-6) and has a 125 amino acid sequence, given in the specification. The invention further relates to: peptide fragments of PAC3 with IL-6-inhibitory activity, formed by addition, suppression and/or replacement of one or more amino acids; a nucleic acid that encodes PAC3 or the fragments of the nucleic acid; antisense oligonucleotides that block transcription or translation of PAC3 or its fragments, able to hybridize to the PAC3 coding nucleic acid; a transgenic, non-human animal that expresses a transgene for PAC3 or its fragments; an expression vector containing PAC3 coding nucleic acid and expression elements; and microorganisms or host cells transformed with the vector containing the PAC3 coding nucleic acid and expression elements. The PAC3 protein, and its active fragments, are used to treat lymphoma, leukaemia, myeloma, carcinoma and sarcoma, other conditions induced by, or associated with, overexpression of interleukin-6, e.g. chronic inflammation, bacterial or viral infections, osteolysis in degenerative diseases and immunological disorders. The nucleic acid that encodes PAC3 can be used for recombinant production of the protein and to prepare transgenic animals, useful as models for studying, in vivo, perturbations of the cell cycle and proliferation caused by abnormal or excessive expression of the PAC3 coding nucleic acid, or its truncated or mutated forms. This sequence represents a human PAC3 protein of the invention.
XX		XX	
SQ	Sequence 118 AA;	SQ	Sequence 125 AA;
	Query Match 59.2%; Score 61; DB 7; Length 118;		Query Match 59.2%; Score 61; DB 7; Length 125;
	Best Local Similarity 57.9%; Pred. No. 0.076;		Best Local Similarity 57.9%; Pred. No. 0.08;
	Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;		Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY	1 GFNETSCLKKLDGPFPE 19	QY	1 GFNETSCLKKLDGPFPE 19
Db	11 GFNETCLVKIITGLLEFE 29	Db	11 GFNETCLVKIITGLLEFE 29
RESULT 7		RESULT 8	
ADH76486		AAU02910	
ID	ADH76486 standard; protein; 125 AA.	ID	AAU02910 standard; protein; 148 AA.
AC	ADH76486;	XX	
XX		AC	AAU02910;
DT	22-APR-2004 (first entry)	XX	
DE	Interleukin-6 inhibiting human PAC3 protein, SEQ ID No 3.	DT	12-SEP-2001 (first entry)
XX		XX	
KW	PAC3; interleukin-6; IL-6; inhibitor; IL-6-inhibitory; lymphoma; leukaemia; myeloma; carcinoma; sarcoma; chronic inflammation; bacterial; viral infection; osteolysis; degenerative disease; immunological disorder; transgenic animal; human.	DE	Angiotensin converting enzyme (ACEV) splice variant protein #10.
KW		XX	
KW		KW	Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonrheumatoid pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
OS	Homo sapiens.	XX	
XX		OS	Homo sapiens.
XX		XX	
PN	FR2833011-A1.	PN	WO200136632-A2.
XX		XX	
XX		XX	
PD	06-JUN-2003.	PD	25-MAY-2001.
XX		XX	
PF	04-DEC-2001; 2001PR-00015623.	XX	
XX		PF	17-NOV-2000; 2000WO-IL000766.
PR	04-DEC-2001; 2001PR-00015623.	XX	
XX		XX	
PA	(UYLY-) UNIV LYON 1 BERNARD CLAUDE.	XX	
PA	(BERA-) CENT BERARD LEON.	XX	
PA	(INRM) INSERM INST NAT SANTE & RECH MEDICALE.	PR	17-NOV-1999; 99IL-00132978.
PA	(HOSP-) HOSPICES CIVILS LYON.	PR	10-DEC-1999; 99IL-00133455.
XX		XX	
PI	Blay JY, Alberti L;	XX	
XX		XX	
XX		XX	
DR	WPI; 2003-471810/45.	XX	
XX		XX	
PT	New protein PAC3, useful for treating cancers, is an inhibitor of	PA	(COMP-) COMPUGEN LTD.

XX PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;
 XX DR WPI; 2001-336004/35.
 XX DR N-PSDB; AAS06010.
 XX PT Novel alternative splicing variants e.g. variant of angiotensin
 PT converting enzyme (ACEV), useful in identifying candidate compounds
 PT capable of binding to the variant and to detect anti-variant antibodies.
 XX PS Claim 4; Fig 10; 519pp; English.
 XX PS
 CC The sequence represents an angiotensin converting enzyme splice variant
 CC (ACEV) polypeptide. The polypeptides of the invention include variants of
 CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
 CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
 CC inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
 CC polypeptide receptor 2. The polypeptides and their associated nucleic
 CC acids are useful for identification of variant sequences and detection of
 CC candidate compounds capable of binding the molecules. The sequences of
 CC the invention can be used in the treatment and diagnosis of various
 CC disorders including cardiovascular diseases such as arteriosclerosis,
 CC myocardial infarction and coronary arterial thrombosis, renal diseases
 CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
 CC immune disorders such as immune complex nephritis, multiple sclerosis,
 CC cancer, sarcoidosis, nonaroidotic pulmonary granulomatous diseases such
 CC as asbestosis and vascular pathologies involving an endothelial
 CC abnormality such as deep vein thrombosis
 XX SQ Sequence 148 AA;
 Query Match 59.2%; Score 61; DB 4; Length 148;
 Best Local Similarity 57.9%; Pred. No. 0.095;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 *QY 1 GFNETSCLKKLADGFFFE 19
 Db 41 GFNEETCLVKIITGLLEFE 59
 RESULT 9
 ADF17513
 ID ADF17513 standard; protein; 157 AA.
 XX AC ADF17513;
 XX DT 12-FEB-2004 (first entry)
 XX DE MB-2 amino acid sequence.
 XX KW protein structure analysis; genetic analysis.
 XX OS Synthetic.
 XX PN W02003091720-A1.
 XX PD 06-NOV-2003.
 XX PF 25-APR-2003; 2003WO-JP005344.
 XX PR 26-APR-2002; 2002JP-00127399.
 XX PA (AJIN) AJINOMOTO CO INC.
 XX PA (UMEY) UMEYAMA H.
 XX PI Umeyama H, Yamada N, Suzuki E, Hirayama K;
 XX DR WPI; 2003-877362/81.
 XX PT Protein structure analysis comprising measuring a fragmented spectrum,
 PT determining classification information, determining information about an
 PT easily cut off region, estimating the stereostructure of the protein and
 PT outputting results.

XX PS Example 5; Fig 18; 103pp; Japanese.
 CC The present invention describes a protein structure analysis method
 CC comprising measuring a fragmented spectrum by dividing the target protein
 CC into several segments, determining the classification information of the
 CC segmented ion corresponding to the amino acid sequence based on the
 CC spectrum, determining an easily cut off region based on the
 CC classification based on the segmented location, estimating the stereo
 CC structure of the protein, and outputting result of estimation data and
 CC easy cut off region information. Also described: (1) a similar method
 CC wherein before estimating the stereo structure, residual solvent
 CC information is determined based on the locations where the amino acid is
 CC in contact with a solvent and on the spectrum and classification
 CC information; (2) a similar method wherein a composite of a protein and a
 CC compound is fragmented, and before estimating the stereo structure the
 CC interface information of mutual effect of the protein and/or compound is
 CC determined; (3) apparatus for carrying out the above methods; and (4)
 CC programs for carrying out the methods. The method can be used for genetic
 CC analysis. The present sequence represents an MB-2 amino acid sequence,
 CC which is used in an example from the present invention.
 XX SQ Sequence 157 AA;
 Query Match 59.2%; Score 61; DB 7; Length 157;
 Best Local Similarity 57.9%; Pred. No. 0.1;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLKKLADGFFFE 19
 Db 50 GFNEETCLVKIITGLLEFE 68
 RESULT 10
 AAR77391
 ID AAR77391 standard; protein; 162 AA.
 XX AC AAR77391;
 XX DT 17-APR-1996 (first entry)
 XX DE Human mutant IL-6a'Cl (amino acids 5-19 and 44-50 deleted).
 XX KW Human interleukin-6; IL-6a'Cl mutant; increased stability; recombinant;
 XX KW production; deletion mutant; amino acids 5-19 and 44-50.
 XX OS Homo sapiens.
 XX PN JP07224097-A.
 XX PD 22-AUG-1995.
 XX PF 08-FEB-1994; 94JP-00014461.
 XX PR 08-FEB-1994; 94JP-00014461.
 XX PA (ASAG) ASAHI GLASS CO LTD.
 XX DR WPI; 1995-325556/42.
 XX DR N-PSDB; AAQ94346.
 XX PT Interleukin-6 mutant, related DNA and expression vectors - has higher
 XX PT stability than natural interleukin-6.
 XX PS Claim 1; Page 14; 18pp; Japanese.
 XX AAQ94346 encodes AAR77391 the human IL-6 deletion mutant IL-6a'Cl, which
 CC lacks the amino acids Gly5-Leu19 and Cys44-Cys50 of the wild type
 CC protein. The cDNA can be used for the recombinant prodn. of IL-6a'Cl,
 CC which has increased stability compared to wild type IL-6
 XX SQ Sequence 162 AA;

```
Query Match          59.2%; Score 61; DB 2; Length 162;
Best Local Similarity 57.9%; Pred. No. 0.1;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
DB 55 GFNEETCLVKIITGLLEFE 73

RESULT 11
AAW00131
ID AAW00131 standard; protein; 162 AA.
XX
AC AAW00131;
XX
DT 09-APR-1997 (first entry)
XX
DE Human interleukin-6 fragment.
XX
KW Secretory; signal peptide; P-factor; multicloning vector; PCR;
KW animal protein; expression; production; recombinant; primer;
KW fission yeast; human; serum albumin; interleukin-6;
KW polymerase chain reaction; Schizosaccharomyces pombe; PO fragment.
XX
OS Homo sapiens.
XX
PN WO9623890-A1.
XX
PD 08-AUG-1996.
XX
PF 01-FEB-1996; 96WO-JP000198.
XX
PR 03-FEB-1995; 95JP-00017167.
XX
PA (ASAG ) ASahi GLASS CO LTD.
XX
PI Hama Y, Tohda H, Tsukamoto H, Nikaido K, Kumagai H;
XX
DR WPI; 1996-371438/37.
XX
PT Schizosaccharomyces pombe secretory signal peptide (P-factor) gene - for
PT production of vectors for expression of animal proteins in a fission
PT yeast, pref. S. pombe, host.
XX
PS Example 4; Page 28-29; 50pp; Japanese.
XX
CC A multicloning vector, comprising the human interleukin-6 (hIL-6) cDNA, a
CC Schizosaccharomyces pombe secretory signal peptide fragment or P-factor
CC fragment (PO fragment) DNA and preferably an animal cell viral promoter
CC sequence and a neomycin resistance gene, can be used for the efficient
CC production of a hIL-6 fragment, i.e. the present sequence, in a fission
CC yeast host, preferably S. pombe, culture
XX
SQ Sequence 162 AA;

Query Match          59.2%; Score 61; DB 2; Length 162;
Best Local Similarity 57.9%; Pred. No. 0.1;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
DB 55 GFNEETCLVKIITGLLEFE 74

RESULT 13
ABU62834
ID ABU62834 standard; protein; 166 AA.
XX
AC ABU62834;
XX
DT 16-SEP-2003 (first entry)
XX
DE Human interleukin-6, IL-6.
XX
KW Human; interleukin-6; IL-6; cytokine; bone homeostasis; Paget's; disease;
KW multiple myeloma; post-menopausal bone loss.
XX
OS Homo sapiens.
XX
PN US2003068300-A1.
XX
PD 10-APR-2003.
XX
PF 19-SEP-2002; 2002US-00246946.
XX
PR 16-AUG-1996; 96US-0024115P.
XX
PR 29-APR-1997; 97US-00841035.
XX
PR 07-FEB-2000; 2000US-00499148.
XX
PA (AMHP ) WYETH.
XX

Query Match          59.2%; Score 61; DB 2; Length 162;
Best Local Similarity 57.9%; Pred. No. 0.1;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
DB 55 GFNEETCLVKIITGLLEFE 73

RESULT 12
AAW00132
ID AAW00132 standard; protein; 163 AA.
XX
AC AAW00132;
XX
DT 09-APR-1997 (first entry)
XX
DE Human interleukin-6 fragment.
```


PI Somers WS, Stahl ML, Seehra JS, Xu G, McDonagh TE, Yu H, Hong J;
 XX WPI; 2003-540877/51.
 XX Computer system useful for identifying agonist or antagonist of
 PT interleukin 6 activity or binding, comprises computer hardware and model
 PT of interleukin 6 structure.
 XX Disclosure; Fig 12; 37pp; English.
 PS
 CC The invention relates to a computer system comprising computer hardware
 CC and model of interleukin (IL)-6 structure, where the model has data set
 CC representing phasing statistics for the native crystal, root mean square
 CC (RMS) deviations from experimental distance restraints (Angstrom), RMS
 CC deviations from idealised covalent geometry, energetics, interhelical and
 CC kink angles and interhelical distances, residues conserved among 9
 CC species of IL-6, as given in specification. Also included are identifying
 CC a species which is an agonist or antagonist of IL-6 activity or binding
 CC using the computer system, an agonist or antagonist species identified by
 CC above mentioned method and identifying a substance that inhibits or
 CC mimics IL-6 activity or binding, using the computer system. IL-6 is a
 CC cytokine involved in bone homeostasis. Increased levels of IL-6 have been
 CC correlated with Paget's disease and multiple myeloma. IL-6 is also
 CC thought to be involved in post-menopausal bone loss. The present sequence
 CC is human IL-6
 XX
 XX Sequence 166 AA;
 SQ
 Query Match 59.2%; Score 61; DB 6; Length 166;
 Best Local Similarity 57.9%; Pred. No. 0.11;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLKKLAGDGFPEFE 19
 DB 59 GFNETCLVKIITGLLEFE 77
 RESULT 14
 ABU62837
 ID ABU62837 standard; protein; 166 AA.
 XX
 AC ABU62837;
 XX
 DT 16-SEP-2003 (first entry)
 XX
 DE Monkey interleukin-6, IL-6.
 XX
 KW Interleukin-6; IL-6; cytokine; bone homeostasis; Paget's; disease;
 KW multiple myeloma; post-menopausal bone loss; monkey.
 XX
 OS Macaca mulatta.
 XX
 PN US2003068300-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 19-SEP-2002; 2002US-00246946.
 XX
 PR 16-AUG-1996; 96US-0024115P.
 PR 29-APR-1997; 97US-00841035.
 PR 07-FEB-2000; 2000US-00499148.
 XX
 PA (AMHP) WYETH.
 XX
 PI Somers WS, Stahl ML, Seehra JS, Xu G, McDonagh TE, Yu H, Hong J;
 XX WPI; 2003-540877/51.
 XX Computer system useful for identifying agonist or antagonist of
 PT interleukin 6 activity or binding, comprises computer hardware and model
 PT of interleukin 6 structure.
 XX
 PS Disclosure; Fig 12; 37pp; English.

XX The invention relates to a computer system comprising computer hardware
 CC and model of interleukin (IL)-6 structure, where the model has data set
 CC representing phasing statistics for the native crystal, root mean square
 CC (RMS) deviations from experimental distance restraints (Angstrom), RMS
 CC deviations from idealised covalent geometry, energetics, interhelical and
 CC kink angles and interhelical distances, residues conserved among 9
 CC species of IL-6, as given in specification. Also included are identifying
 CC a species which is an agonist or antagonist of IL-6 activity or binding
 CC using the computer system, an agonist or antagonist species identified by
 CC above mentioned method and identifying a substance that inhibits or
 CC mimics IL-6 activity or binding, using the computer system. IL-6 is a
 CC cytokine involved in bone homeostasis. Increased levels of IL-6 have been
 CC correlated with Paget's disease and multiple myeloma. IL-6 is also
 CC thought to be involved in post-menopausal bone loss. The present sequence
 CC is an IL-6 protein from a species other than human, used in the
 CC determination of the structure of human IL-6
 XX
 XX Sequence 166 AA;
 SQ
 Query Match 59.2%; Score 61; DB 6; Length 166;
 Best Local Similarity 57.9%; Pred. No. 0.11;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLKKLAGDGFPEFE 19
 DB 59 GFNETCLVKIITGLLEFE 77
 RESULT 15
 ADC20004
 ID ADC20004 standard; protein; 166 AA.
 XX
 AC ADC20004;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Rhesus monkey interleukin-6, IL-6.
 XX
 KW rhesus monkey; crystal; interleukin-6; IL-6;
 KW IL-6/IL-6 receptor interaction.
 XX
 OS Macaca mulatta.
 XX
 PN US6461604-B1.
 XX
 PD 08-OCT-2002.
 XX
 PF 07-FEB-2000; 2000US-00499148.
 XX
 PR 16-AUG-1996; 96US-0024115P.
 PR 29-APR-1997; 97US-00841035.
 XX
 PA (GEMY) GENETICS INST LLC.
 XX
 PI Somers WS, Stahl ML, Seehra JS, Xu G, McDonagh TE, Yu H, Hong J;
 XX WPI; 2003-719565/68.
 XX
 DR Crystalline human interleukin-6, useful for identifying IL-6/IL-6
 XX receptor interactions, and for identifying agonists and antagonists of
 PT such interactions, has diffracting crystals of a specific space group.
 PT
 XX Disclosure; SEQ ID NO 4; 30pp; English.
 PS
 CC The invention relates to crystalline human interleukin-6 (IL-6). The
 CC crystalline form of IL-6 is useful for identifying IL-6/IL-6 receptor
 CC interactions, and for identifying agonists and antagonists of the
 CC interactions. Crystalline IL-6 structure enables effective study of its
 CC interactions with its receptor. The present sequence represents the amino
 CC acid sequence of rhesus monkey interleukin-6, IL-6.
 XX
 XX Sequence 166 AA;
 SQ

Query Match 59.2%; Score 61; DB 7; Length 166;
 Best Local Similarity 57.9%; Pred.No. 0.11;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GENETSCCLKLADGFFFE 19
 ||| :|| : |||
 Db 59 GFNEDTCLVKIITGLLEFE 77

Search completed: March 30, 2005, 22:01:42
 Job time : 22.0448 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005: Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2005, 21:58:00 ; Search time 5.02691 Seconds
(without alignments)
282.148 Million cell updates/sec

Title: US-10-828-343-2_COPY_87_105
Perfect score: 103
Sequence: 1 GFNETSCLKKLADGFFFE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	185	3	US-09-122-443-16
2	103	100.0	185	4	US-09-558-089-16
3	103	100.0	185	4	US-09-558-087-16
4	103	100.0	185	4	US-09-558-474-16
5	103	100.0	204	3	US-09-230-637-25
6	103	100.0	204	3	US-09-230-371A-26
7	61	59.2	89	4	US-09-687-637B-36
8	61	59.2	89	4	US-09-687-637B-37
9	61	59.2	89	4	US-09-687-637B-38
10	61	59.2	162	2	US-08-716-317-10
11	61	59.2	163	2	US-08-716-317-15
12	61	59.2	164	1	US-08-318-193-60
13	61	59.2	166	4	US-09-499-148-1
14	61	59.2	166	4	US-09-499-148-4
15	61	59.2	167	1	US-08-246-427A-2
16	61	59.2	167	2	US-08-766-620-2
17	61	59.2	167	5	PCT-US95-06094-2
18	61	59.2	172	3	US-08-149-101A-21
19	61	59.2	172	5	PCT-US94-12873-21
20	61	59.2	174	3	US-08-149-101A-20
21	61	59.2	174	5	PCT-US94-12873-20
22	61	59.2	183	1	US-08-009-973-1
23	61	59.2	184	1	US-08-567-047-2
24	61	59.2	184	2	US-08-693-182-2
25	61	59.2	184	2	US-08-567-048-2
26	61	59.2	184	2	US-09-008-482-2
27	61	59.2	184	2	US-08-945-529-8

28	61	59.2	184	2	US-08-945-529-9	Sequence 9, Appli
29	61	59.2	184	2	US-08-945-529-10	Sequence 10, Appl
30	61	59.2	184	2	US-08-945-529-11	Sequence 11, Appl
31	61	59.2	184	2	US-08-945-529-12	Sequence 12, Appl
32	61	59.2	184	3	US-08-149-101A-17	Sequence 17, Appl
33	61	59.2	184	3	US-08-149-101A-22	Sequence 22, Appl
34	61	59.2	184	4	US-09-559-950A-1	Sequence 1, Appli
35	61	59.2	184	5	PCT-US94-12873-17	Sequence 17, Appl
36	61	59.2	184	5	PCT-US94-12873-22	Sequence 22, Appl
37	61	59.2	184	6	5186931-1	Patent No. 5186931
38	61	59.2	184	6	5186931-1	Patent No. 5186931
39	61	59.2	185	1	US-07-632-070B-1	Sequence 1, Appli
40	61	59.2	185	1	US-07-918-181A-2	Sequence 2, Appli
41	61	59.2	185	1	US-07-918-181A-4	Sequence 4, Appli
42	61	59.2	185	1	US-07-918-181A-6	Sequence 6, Appli
43	61	59.2	185	1	US-07-918-181A-8	Sequence 8, Appli
44	61	59.2	185	1	US-08-231-575-2	Sequence 2, Appli
45	61	59.2	185	1	US-08-231-575-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-122-443-16
; Sequence 16, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-16

Query Match 100.0%; Score 103; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFNETSCLKKLADGFFFE 19
DB 68 GFNETSCLKKLADGFFFE 86

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RESULT 2
US-09-558-089-16
; Sequence 16, Application US/09558089
; Patent No. 6479634
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,089
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/122,443
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-089-16
Query Match 100.0%; Score 103; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGPFPE 19
Db 68 GNETSCLKKLADGPFPE 86

RESULT 3
US-09-558-087-16
; Sequence 16, Application US/09558087
; Patent No. 6495667
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,474
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-089-16
Query Match 100.0%; Score 103; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGPFPE 19
Db 68 GNETSCLKKLADGPFPE 86

RESULT 4
US-09-558-474-16
; Sequence 16, Application US/09558474
; Patent No. 6835825
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,474
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-087-16
Query Match 100.0%; Score 103; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGPFPE 19
Db 68 GNETSCLKKLADGPFPE 86
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558,087
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-087-16
Query Match 100.0%; Score 103; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGPFPE 19
Db 68 GNETSCLKKLADGPFPE 86

RESULT 4
US-09-558-474-16
; Sequence 16, Application US/09558474
; Patent No. 6835825
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,474
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-087-16
Query Match 100.0%; Score 103; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGPFPE 19
Db 68 GNETSCLKKLADGPFPE 86
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; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-474-16

Query Match      100.0%; Score 103; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 68 GFNETSCLKKLADGFFFE 86

RESULT 5
US-09-230-637-25
; Sequence 25, Application US/09230637
; Patent No. 6264958
; GENERAL INFORMATION:
; APPLICANT: Hayward, Gary
; APPLICANT: Nicholas, John
; APPLICANT: Hardwick, J. Marie
; APPLICANT: Reitz, Marvin
; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
; FILE REFERENCE: 1107.78372
; CURRENT APPLICATION NUMBER: US/09/230,637
; CURRENT FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/022,591
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: PCT US 97/12931
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpes-like virus
US-09-230-637-25

Query Match      100.0%; Score 103; DB 3; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 87 GFNETSCLKKLADGFFFE 105

RESULT 6
US-09-230-371A-26
; Sequence 26, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US97/13346
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-26

Query Match      100.0%; Score 103; DB 3; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 87 GFNETSCLKKLADGFFFE 105

RESULT 7
US-09-687-637B-36
; Sequence 36, Application US/09687637B
; Patent No. 6610285
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/09/687,637B
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Cercopithecus torquatus atys
US-09-687-637B-36

Query Match      59.2%; Score 61; DB 4; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 54 GFNETCLVKIITGLLEFE 72

RESULT 8
US-09-687-637B-37
; Sequence 37, Application US/09687637B
; Patent No. 6610285
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/09/687,637B
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-687-637B-37

Query Match      59.2%; Score 61; DB 4; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 54 GFNETCLVKIITGLLEFE 72

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RESULT 9
US-09-687-637B-38
; Sequence 38, Application US/09687637B
; Patent No. 6610285
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/09/687,637B
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-687-637B-38

Query Match 59.2%; Score 61; DB 4; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGFFFE 19
||||:|:|:|
DB 54 GFNEETCLVKIITGLLEFE 72

RESULT 10
US-08-716-317-10
; Sequence 10, Application US/08716317
; Patent No. 5919654
; GENERAL INFORMATION:
; APPLICANT: HAMA, YUKO
; APPLICANT: TOHDA, HIDEKI
; APPLICANT: TSUKAMOTO, HIROKO
; APPLICANT: NIKAIIDO, KIYOKAZU
; APPLICANT: KUMAGAI, HIROMICHI
; TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
; TITLE OF INVENTION: VECTOR CONTAINING IT
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,317
FILING DATE: 02-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
FILING DATE: 03-FEB-1996
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-716-317-10

Query Match 59.2%; Score 61; DB 2; Length 162;
Best Local Similarity 57.9%; Pred. No. 0.022;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGFFFE 19
||||:|:|:|
DB 55 GFNEETCLVKIITGLLEFE 73

RESULT 11
US-08-716-317-15
; Sequence 15, Application US/08716317
; Patent No. 5919654
; GENERAL INFORMATION:
; APPLICANT: HAMA, YUKO
; APPLICANT: TOHDA, HIDEKI
; APPLICANT: TSUKAMOTO, HIROKO
; APPLICANT: NIKAIIDO, KIYOKAZU
; APPLICANT: KUMAGAI, HIROMICHI
; TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
; TITLE OF INVENTION: VECTOR CONTAINING IT
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,317
FILING DATE: 02-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
FILING DATE: 03-FEB-1996
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-716-317-15

Query Match 59.2%; Score 61; DB 2; Length 163;
Best Local Similarity 57.9%; Pred. No. 0.022;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLDGPFPE 19
Db 56 GFNEETCLVKIITGLLEFE 74

RESULT 12

US-08-318-193-60
Sequence 60, Application US/08318193

Patent No. 5641663

GENERAL INFORMATION:

APPLICANT: GARVIN, Robert T.

APPLICANT: MALEK, Lawrence T.

TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION

TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY

TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS

TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/318,193

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US/07/935,314

FILING DATE:

ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: US 07/224,568

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 18740/116 CACO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 164 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-318-193-60

Query Match 59.2%; Score 61; DB 1; Length 164;

Best Local Similarity 57.9%; Pred. No. 0.022;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLDGPFPE 19
Db 57 GFNEETCLVKIITGLLEFE 75

RESULT 13

US-09-499-148-1

Sequence 1, Application US/09499148

Patent No. 6461604

GENERAL INFORMATION:

APPLICANT: SOMERS, WILLIAM

APPLICANT: STAHL, MARK L.

APPLICANT: SEEHRA, JASBIR S.

APPLICANT: XU, GUANG-YI

APPLICANT: MCCONAGH, THOMAS E.

APPLICANT: YU, HSIANG-AI

APPLICANT: HONG, JIN

TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6

FILE REFERENCE: 50657-05278USC1

CURRENT APPLICATION NUMBER: US/09/499,148

CURRENT FILING DATE: 2000-02-07

PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115

PRIOR FILING DATE: 1997-4-28 AND 1996-8-16

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 166

TYPE: PRT

ORGANISM: Homo sapiens

US-09-499-148-1

Query Match

Best Local Similarity 59.2%; Score 61; DB 4; Length 166;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLDGPFPE 19
Db 59 GFNEETCLVKIITGLLEFE 77

RESULT 14

US-09-499-148-4

Sequence 4, Application US/09499148

Patent No. 6461604

GENERAL INFORMATION:

APPLICANT: SOMERS, WILLIAM

APPLICANT: STAHL, MARK L.

APPLICANT: SEEHRA, JASBIR S.

APPLICANT: XU, GUANG-YI

APPLICANT: MCCONAGH, THOMAS E.

APPLICANT: YU, HSIANG-AI

APPLICANT: HONG, JIN

TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6

FILE REFERENCE: 50657-05278USC1

CURRENT APPLICATION NUMBER: US/09/499,148

CURRENT FILING DATE: 2000-02-07

PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115

PRIOR FILING DATE: 1997-4-28 AND 1996-8-16

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

SEQ ID NO 4

LENGTH: 166

TYPE: PRT

ORGANISM: Macaca mulatta

US-09-499-148-4

Query Match

Best Local Similarity 59.2%; Score 61; DB 4; Length 166;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLDGPFPE 19
Db 59 GFNEETCLVKIITGLLEFE 77

RESULT 15

US-08-246-427A-2

Sequence 2, Application US/08246427A

Patent No. 5641657

GENERAL INFORMATION:

APPLICANT: RUBEN, ET AL.

TITLE OF INVENTION: Interleukin-6 Splice Variant

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

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; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,427A
; FILING DATE: Submitted herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/246,427
; FILING DATE: MAY 19, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-246-427A-2

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Query Match      59.2%; Score 61; DB 1; Length 167;
Best Local Similarity 57.9%; Pred. No. 0.022;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY      1 GFNETSCLKKLADGFFFE 19
Db      60 GFNETCLVKIITGLLEFE 78

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Search completed: March 30, 2005, 22:11:03
Job time : 6.02691 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:49:40 ; Search time 16.1031 Seconds
(without alignments)
390.664 Million cell updates/sec

Title: US-10-828-343-2_COPY_87_105
Perfect score: 103
Sequence: 1 GFNETSCLKKLADGPFPEFE 19

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	59.2	89	14	US-10-440-066-36
2	61	59.2	89	14	US-10-440-066-37
3	61	59.2	89	14	US-10-440-066-38
4	61	59.2	166	14	US-10-246-946-1
5	61	59.2	166	14	US-10-246-946-4
6	61	59.2	183	16	US-10-658-834A-198
7	61	59.2	183	16	US-10-658-834A-217
8	61	59.2	183	16	US-10-658-834A-896
9	61	59.2	183	16	US-10-658-834A-897
10	61	59.2	183	16	US-10-658-834A-898
11	61	59.2	183	16	US-10-658-834A-899
12	61	59.2	183	16	US-10-658-834A-900
13	61	59.2	183	16	US-10-658-834A-901

14	61	59.2	183	16	US-10-658-834A-902	Sequence 902, App
15	61	59.2	183	16	US-10-658-834A-903	Sequence 903, App
16	61	59.2	183	16	US-10-658-834A-904	Sequence 904, App
17	61	59.2	183	16	US-10-658-834A-905	Sequence 905, App
18	61	59.2	183	16	US-10-658-834A-906	Sequence 906, App
19	61	59.2	183	16	US-10-658-834A-907	Sequence 907, App
20	61	59.2	183	16	US-10-658-834A-908	Sequence 908, App
21	61	59.2	183	16	US-10-658-834A-914	Sequence 914, App
22	61	59.2	183	16	US-10-658-834A-915	Sequence 915, App
23	61	59.2	183	16	US-10-658-834A-916	Sequence 916, App
24	61	59.2	183	16	US-10-658-834A-917	Sequence 917, App
25	61	59.2	183	16	US-10-658-834A-918	Sequence 918, App
26	61	59.2	183	16	US-10-658-834A-919	Sequence 919, App
27	61	59.2	183	16	US-10-658-834A-920	Sequence 920, App
28	61	59.2	183	16	US-10-658-834A-921	Sequence 921, App
29	61	59.2	183	16	US-10-658-834A-922	Sequence 922, App
30	61	59.2	183	16	US-10-658-834A-923	Sequence 923, App
31	61	59.2	183	16	US-10-658-834A-924	Sequence 924, App
32	61	59.2	183	16	US-10-658-834A-925	Sequence 925, App
33	61	59.2	183	16	US-10-658-834A-926	Sequence 926, App
34	61	59.2	183	16	US-10-658-834A-927	Sequence 927, App
35	61	59.2	183	16	US-10-658-834A-928	Sequence 928, App
36	61	59.2	183	16	US-10-658-834A-929	Sequence 929, App
37	61	59.2	183	16	US-10-658-834A-930	Sequence 930, App
38	61	59.2	183	16	US-10-658-834A-931	Sequence 931, App
39	61	59.2	183	16	US-10-658-834A-932	Sequence 932, App
40	61	59.2	183	16	US-10-658-834A-933	Sequence 933, App
41	61	59.2	183	16	US-10-658-834A-934	Sequence 934, App
42	61	59.2	183	16	US-10-658-834A-935	Sequence 935, App
43	61	59.2	183	16	US-10-658-834A-936	Sequence 936, App
44	61	59.2	183	16	US-10-658-834A-937	Sequence 937, App
45	61	59.2	183	16	US-10-658-834A-938	Sequence 938, App

ALIGNMENTS

RESULT 1
US-10-440-066-36
; Sequence 36, Application US/10440066
; Publication No. US20030180256A1
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/10/440,066
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US/09/687,637
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Cercosporium torquatus atys
US-10-440-066-36

Query Match 59.2%; Score 61; DB 14; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.02;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFPEFE 19
|||||:|:|:|
Db 54 GFNETCLVKIITGLLEFE 72

RESULT 2
US-10-440-066-37
; Sequence 37, Application US/10440066

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; Publication No. US20030180256A1
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/10/440,066
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US/09/687,637
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-440-066-37

Query Match      59.2%; Score 61; DB 14; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.02;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFEE 19
Db 54 GFNETCLVKIITGLLEFE 72

RESULT 3
US-10-440-066-38
; Sequence 38, Application US/10440066
; Publication No. US20030180256A1
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/10/440,066
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US/09/687,637
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-066-38

Query Match      59.2%; Score 61; DB 14; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.02;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFEE 19
Db 54 GFNETCLVKIITGLLEFE 72

RESULT 4
US-10-246-946-1
; Sequence 1, Application US/10246946
; Publication No. US20030068300A1
; GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; APPLICANT: STAHL, MARK L.
; APPLICANT: SEEHRA, JASBIR S.
; APPLICANT: MCCONAGH, THOMAS E.
; APPLICANT: YU, HSIANG-AI
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/10/440,066
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US/09/687,637
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-066-38

Query Match      59.2%; Score 61; DB 14; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.02;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFEE 19
Db 54 GFNETCLVKIITGLLEFE 72

RESULT 5
US-10-246-946-4
; Sequence 4, Application US/10246946
; Publication No. US20030068300A1
; GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; APPLICANT: STAHL, MARK L.
; APPLICANT: SEEHRA, JASBIR S.
; APPLICANT: XU, GUANG-YI
; APPLICANT: MCCONAGH, THOMAS E.
; APPLICANT: YU, HSIANG-AI
; APPLICANT: HONG, JIN
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/10/246,946
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 09/499,148, 08/841,035 AND 60/024,115
; PRIOR FILING DATE: 2000-2-7, 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-246-946-4

Query Match      59.2%; Score 61; DB 14; Length 166;
Best Local Similarity 57.9%; Pred. No. 0.041;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFEE 19
Db 59 GFNETCLVKIITGLLEFE 77

RESULT 6
US-10-658-834A-198
; Sequence 198, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
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; APPLICANT: YU, HSIANG-AI
; APPLICANT: HONG, JIN
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/10/246,946
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 09/499,148, 08/841,035 AND 60/024,115
; PRIOR FILING DATE: 2000-2-7, 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-946-1

Query Match      59.2%; Score 61; DB 14; Length 166;
Best Local Similarity 57.9%; Pred. No. 0.041;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFEE 19
Db 59 GFNETCLVKIITGLLEFE 77
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RESULT 5
US-10-246-946-4
; Sequence 4, Application US/10246946
; Publication No. US20030068300A1
; GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; APPLICANT: STAHL, MARK L.
; APPLICANT: SEEHRA, JASBIR S.
; APPLICANT: XU, GUANG-YI
; APPLICANT: MCCONAGH, THOMAS E.
; APPLICANT: YU, HSIANG-AI
; APPLICANT: HONG, JIN
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/10/246,946
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 09/499,148, 08/841,035 AND 60/024,115
; PRIOR FILING DATE: 2000-2-7, 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-246-946-4

Query Match      59.2%; Score 61; DB 14; Length 166;
Best Local Similarity 57.9%; Pred. No. 0.041;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFEE 19
Db 59 GFNETCLVKIITGLLEFE 77
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RESULT 6
US-10-658-834A-198
; Sequence 198, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
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```

; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank CAA00839
; DATABASE ENTRY DATE: 1993-12-03
US-10-658-834A-198

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Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 GFNETSCLKKLADGFFFE 19
||||:|:|:|
Db 76 GFNEETCLVKIITGLLEFE 94

```

RESULT 7

```

US-10-658-834A-217
; Sequence 217, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAD13886
; DATABASE ENTRY DATE: 1993-06-28
US-10-658-834A-217

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Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 GFNETSCLKKLADGFFFE 19
||||:|:|:|
Db 76 GFNEETCLVKIITGLLEFE 94

```

RESULT 8

```

US-10-658-834A-896
; Sequence 896, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila

```

```

; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-896

```

```

Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 GFNETSCLKKLADGFFFE 19
||||:|:|:|
Db 76 GFNEETCLVKIITGLLEFE 94

```

RESULT 9

```

US-10-658-834A-897
; Sequence 897, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 897
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-897

```

```

Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 GFNETSCLKKLADGFFFE 19
||||:|:~|:|
Db 76 GFNEETCLVKIITGLLEFE 94

```

RESULT 10

```

US-10-658-834A-898
; Sequence 898, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel

```

```
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 898
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-898

Query Match          59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFPE 19
    ||||:|:|:|
Db 76 GFNEETCLVKIITGLLEPE 94

RESULT 11
US-10-658-834A-899
; Sequence 899, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 899
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-899

Query Match          59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFPE 19
    ||||:|:|:|
Db 76 GFNEETCLVKIITGLLEPE 94

RESULT 12
US-10-658-834A-900
; Sequence 900, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
```

```
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 900
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-900

Query Match          59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFPE 19
    ||||:|:|:|
Db 76 GFNEETCLVKIITGLLEPE 94

RESULT 13
US-10-658-834A-901
; Sequence 901, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 901
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-901

Query Match          59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFPE 19
    ||||:|:|:|
Db 76 GFNEETCLVKIITGLLEPE 94

RESULT 14
US-10-658-834A-902
; Sequence 902, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
```

```
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 902
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-658-834A-902
```

```
Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
   ||||:||||:
Db 76 GFNETCLVKIITGLLEFE 94
```

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RESULT 15
US-10-658-834A-903
; Sequence 903, Application US/10658834A
; Publication No. US20040112977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 903
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-658-834A-903
```

```
Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
   ||||:||||:
Db 76 GFNETCLVKIITGLLEFE 94
```

Search completed: March 30, 2005, 22:09:56
Job time : 16.1031 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2005, 21:47:50 ; Search time 4.5157 Seconds
(without alignments)
404.837 Million cell updates/sec

Title: US-10-828-343-2_COPY_87_105
Perfect score: 103
Sequence: 1 GFNETSCLKLADGFFFE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	59.2	212	1	IVHUB2
2	55	53.4	208	2	T09216
3	53	51.5	212	2	I46590
4	53	51.5	212	2	I46621
5	51	49.5	207	2	I46084
6	49	47.6	211	2	A34247
7	48.5	47.1	196	2	C95322
8	48	46.6	162	2	H83786
9	47	45.6	211	1	ICM86
10	47	45.6	745	2	T05375
11	46	44.7	208	1	S29549
12	46	44.7	568	2	C82379
13	45	43.7	484	2	F71061
14	44	42.7	282	2	D70149
15	44	42.7	454	2	T27249
16	44	42.7	1893	2	T22661
17	44	42.7	2875	1	RRVUTW
18	44	42.7	4196	2	T43274
19	43.5	42.2	233	2	AC2205
20	43	41.7	157	2	H69203
21	43	41.7	208	1	A56610
22	43	41.7	231	2	H83664
23	42.5	41.3	492	2	T30066
24	42	40.8	180	2	H72402
25	42	40.8	219	2	H88101
26	42	40.8	364	2	T23819
27	42	40.8	445	2	G98290
28	42	40.8	445	2	AC2993
29	42	40.8	512	2	S47900

ALIGNMENTS

RESULT 1

IVHUB2

Interleukin-6 precursor [validated] - human

N;Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-cell

on factor

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004

C;Accession: A32648; A25692; A26966; A3515; A25801; A25921; I52193; I56003; A27601; B27

R;Yasukawa, K.; Hirano, T.; Watanabe, Y.; Murakami, K.; Matsuda, T.; Nakai, S.; Kishimoto,

EMBO J. 6, 2939-2945, 1987

A;Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene

A;Reference number: A32648; MUID:88082664; PMID:3500852

A;Accession: A32648

A;Molecule type: DNA

A;Residues: 1-212 <YAS>

A;Cross-references: UNIPROT:P05231; GB:Y00081; NID:G29494; PIDN:CAA68278.1; PID:G29495

A;Note: the authors translated the codon CAG for residue 130 as Glu

R;Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.

EMBO J. 5, 2529-2537, 1986

A;Title: Structure and expression of cDNA and genes for human interferon-beta-2, a distri

A;Reference number: A91051; MUID:87053818; PMID:3023045

A;Accession: A25692

A;Molecule type: mRNA

A;Residues: 1-212 <ZIL>

A;Cross-references: GB:X04430; NID:G32673; PIDN:CAA28026.1; PID:G32674

R;Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwamura,

I, T.; Kishimoto, T.

Nature 324, 73-76, 1986

A;Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymphocyt

A;Reference number: A93387; MUID:87065033; PMID:3491322

A;Accession: A26966

A;Molecule type: mRNA

A;Residues: 1-212 <HIR>

A;Cross-references: GB:X04602; NID:G33849; PIDN:CAA28268.1; PID:G33850

R;Tonouchi, N.; Miwa, K.; Kasayama, H.; Matsui, H.

Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989

A;Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization of t

A;Reference number: A3515; MUID:89391958; PMID:2789513

A;Accession: A3515

A;Molecule type: mRNA

A;Residues: 1-212 <TON>

A;Cross-references: GB:M29150; NID:G186349; PIDN:AAA59154.1; PID:G307063

R;Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.

Eur. J. Biochem. 159, 625-632, 1986

A;Title: Structural analysis of the sequence coding for an inducible 26-kDa protein in h

A;Reference number: A25801; MUID:87004683; PMID:3758081

A;Accession: A25801

A;Molecule type: DNA: mRNA

A;Residues: 1-212 <HAE>

A;Cross-references: GB:X04403

A;Experimental source: fibroblast

R;May, L.T.; Helfgott, D.C.; Sehgal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
A>Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
A:Reference number: A25921; MUID:87067433; PMID:3538015
A:Accession: A25921
A:Molecule type: mRNA
A:Residues: 1-212 <MAY>
A:Cross-references: GB:M14584; NID:g184628; PIDN:AAA52728.1; PID:g306910
R:Wong, G.G.; Witek-Giannotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
Behring Inst. Mitt. 83, 40-47, 1988
A>Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
A:Reference number: I52193; MUID:89193317; PMID:3266463
A:Accession: I52193
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-212 <NON>
A:Cross-references: GB:IM54894; NID:g186351; PIDN:AAAC41704.1; PID:g186352
R:Brakenhoff, J.P.; de Groot, E.R.; Evers, R.P.; Pannekoek, H.; Aarden, L.A.
J. Immunol. 139, 4116-4121, 1987
A>Title: Molecular cloning and expression of hybridoma growth factor in Escherichia coli
A:Reference number: I56003; MUID:88088768; PMID:3320204
A:Accession: I56003
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-212 <BRA>
A:Cross-references: GB:M18403; NID:g184631; PIDN:AAA52729.1; PID:g306911
R:Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
J. Immunol. 140, 1534-1541, 1988
A>Title: Separation and comparison of two monokines with lymphocyte-activating factor activity
A:Reference number: A92816; MUID:88154445; PMID:3279116
A:Accession: A27601
A:Molecule type: protein
A:Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VAN1>
A:Accession: B27601
A:Molecule type: protein
A:Residues: 30-56, 'XX', 59-61, 'X', 63 <VA2>
R:Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
J. Immunol. 144, 1808-1816, 1990
A>Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved in human lung fibroblast cell growth
A:Reference number: A60400; MUID:90171574; PMID:2307841
A:Accession: A60400
A:Molecule type: protein
A:Residues: 30-43 <YAM>
R:Hitano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, M.
Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
A>Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and its cDNA
A:Reference number: A29085; MUID:87092370; PMID:3491991
A:Accession: A29085
A:Molecule type: protein
A:Residues: 29-42 <HIR2>
R:Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Aizawa, Y.
Anticancer Res. 11, 961-968, 1991
A>Title: Purification and characterization of human fibroblast derived differentiation factor 1
A:Reference number: A61159; MUID:91290785; PMID:1648338
A:Accession: A61159
A:Molecule type: protein
A:Residues: 30-42 <NOD>
A:Experimental source: fibroblast
R:Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A.
J. Mol. Cell. Immunol. 4, 203-212, 1989
A>Title: Interleukin 6 is the principal cytokine in the differentiation of human T lymphocytes
A:Reference number: A61462; MUID:90121567; PMID:2610854
A:Accession: A61462
A:Molecule type: protein
A:Residues: 28-48 <MIN>
A:Experimental source: leukocyte-conditioned medium
R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal, P.B.
Cytokine 3, 204-211, 1991
A>Title: Marked cell-type-specific differences in glycosylation of human interleukin-6
A:Reference number: A48419; MUID:91355644; PMID:1883960
A:Accession: A48419
A:Molecule type: protein
A:Residues: 30-37, 'X', 39-40 <MAY2>
A:Experimental source: FS-4 fibroblasts

A>Note: sequence extracted from NCBI backbone
A>Note: this 28-30K form contained both N-linked and O-linked carbohydrate; a 25K form contained only N-linked carbohydrate
A:Accession: C48419
A:Molecule type: protein
A:Residues: 28-40 <MAY3>
A:Experimental source: FS-4 fibroblasts
A>Note: sequence extracted from NCBI backbone (NCBIP:63787)
A>Note: this 23-25K form contained O-linked but not N-linked carbohydrate
R:Orlita, T.; Oneda, M.; Hasegawa, M.; Kuboniva, M.; Esaki, K.; Ochi, N.
J. Biochem. 115, 345-350, 1994
A>Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 produced in CHO cells
A:Reference number: JX0305; MUID:94266765; PMID:8206884
A:Contents: annotation; modified sites in recombinant protein from CHO cells
R:Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
Arch. Biochem. Biophys. 272, 144-151, 1989
A>Title: Disulfide structures of human interleukin-6 are similar to those of human granulocyte colony-stimulating factor
A:Reference number: S04981; MUID:89286115; PMID:2472117
A:Contents: annotation; disulfide bonds in recombinant protein
R:Rock, F.L.; Li, X.; Chong, P.; Ida, N.; Klein, M.
Biochemistry 33, 5146-5154, 1994
A>Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
A:Reference number: A54253; MUID:94227044; PMID:8172889
A:Contents: annotation; lability and functional significance of each disulfide bond
C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factors (IL-1, IL-3, IL-6, IL-11, IL-12, IL-13, IL-15, IL-18, IL-21, IL-23, IL-25, IL-27, IL-28, IL-29, IL-30, IL-31, IL-32, IL-33, IL-34, IL-35, IL-36, IL-37, IL-38, IL-39, IL-40, IL-41, IL-42, IL-43, IL-44, IL-45, IL-46, IL-47, IL-48, IL-49, IL-50, IL-51, IL-52, IL-53, IL-54, IL-55, IL-56, IL-57, IL-58, IL-59, IL-60, IL-61, IL-62, IL-63, IL-64, IL-65, IL-66, IL-67, IL-68, IL-69, IL-70, IL-71, IL-72, IL-73, IL-74, IL-75, IL-76, IL-77, IL-78, IL-79, IL-80, IL-81, IL-82, IL-83, IL-84, IL-85, IL-86, IL-87, IL-88, IL-89, IL-90, IL-91, IL-92, IL-93, IL-94, IL-95, IL-96, IL-97, IL-98, IL-99, IL-100, IL-101, IL-102, IL-103, IL-104, IL-105, IL-106, IL-107, IL-108, IL-109, IL-110, IL-111, IL-112, IL-113, IL-114, IL-115, IL-116, IL-117, IL-118, IL-119, IL-120, IL-121, IL-122, IL-123, IL-124, IL-125, IL-126, IL-127, IL-128, IL-129, IL-130, IL-131, IL-132, IL-133, IL-134, IL-135, IL-136, IL-137, IL-138, IL-139, 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RESULT 3

I46590
interleukin 6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46590
R;Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A;Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conceptuses
A;Reference number: I46590; MUID:92360284; PMID:1497880
A;Accession: I46590
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <MAT>
A;Cross-references: UNIPROT:P26893; GB:M80258; NID:g164514; PIDN:AACT27127.1; PID:g164514
C;Genetics:
A;Gene: IL-6
C;Superfamily: interleukin-6

Query Match 51.5%; Score 53; DB 2; Length 212;
Best Local Similarity 42.1%; Pred. No. 0.51;
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Db 105 GFNQETCLMRITTTGLVEFQ 123

RESULT 4

I46621
prointerleukin 6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46621
R;Richards, C.; Saklatva, J.
Cytokine 3, 269-276, 1991
A;Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of the cDNA
A;Reference number: I46621; MUID:91338547; PMID:1873476
A;Accession: I46621
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <RTC>
A;Cross-references: UNIPROT:P26893; GB:M86722; NID:g164624; PIDN:AACT37333.1; PID:g164624
C;Genetics:
A;Gene: IL6
C;Superfamily: interleukin-6

Query Match 51.5%; Score 53; DB 2; Length 212;
Best Local Similarity 42.1%; Pred. No. 0.51;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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RESULT 5

I46084
interleukin 6 - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I46084
R;Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993
A;Title: Molecular cloning and characterization of a cDNA encoding feline interleukin-6.
A;Reference number: I46084; MUID:94052249; PMID:8234373
A;Accession: I46084
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-207 <BRA>
A;Cross-references: UNIPROT:P41683; GB:L16914; NID:g438519; PIDN:AAA16620.1; PID:g438520
C;Superfamily: interleukin-6

Query Match 49.5%; Score 51; DB 2; Length 207;
Best Local Similarity 42.1%; Pred. No. 1;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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Db 101 GFNQETCLTRITTTGLQEFQ 119

RESULT 6

A34247
interleukin-6 precursor - rat
N;Alternate names: IL-6
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34247
R;Northemann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989
A;Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derived cells
A;Reference number: A34247; MUID:89380206; PMID:2789217
A;Accession: A34247
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-211 <NOR>
A;Cross-references: UNIPROT:P20607; GB:M26744; NID:g204915; PIDN:AAA77659.1; PID:g204916
C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match 47.6%; Score 49; DB 2; Length 211;
Best Local Similarity 44.4%; Pred. No. 2.2;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 18
||||: |||: |||:
Db 103 GYNQETCLLKICSGLLLEF 120

RESULT 7

C95322
hypothetical protein Sma0882 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmi
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95322
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, P.; Bowse, P.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Welle, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95322
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-196 <KUR>
A;Cross-references: UNIPROT:Q92ZK2; GB:AE006469; PIDN:AAK65141.1; PID:g14523582; GSPDB:GSPDB:R;Galibert, P.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, H.; Rebaud, P.; Vandendol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.; A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C;Contents: annotation
C;Genetics:
A;Gene: Sma0882
A;Genome: plasmid

Query Match 47.1%; Score 48.5; DB 2; Length 196;

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Best Local Similarity 58.8%; Pred. No. 2.5;
Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 FNETSCLKKLADGFFEF 18
Db 86 FNSNRCL-IADGFEF 101

RESULT 8
H83786
hypothetical protein BH1096 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
A:Accession: H83786
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: H83786
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-162 <STO>
A:Cross-references: UNIPROT:Q9KDW5; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA048
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1096

Query Match 46.6%; Score 48; DB 2; Length 162;
Best Local Similarity 56.7%; Pred. No. 2.5;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 TSCLKKLADGFFEE 19
Db 31 TSMIEIGADGFFEE 45

RESULT 9
ICWS6
interleukin-6 precursor - mouse
A:Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocy
acytoma growth factor
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
A:Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799; S10
R:Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
J. Immunol. 141, 3875-3881, 1988
A:Title: Genomic structure of the murine IL-6 gene. High degree conservation of potentia
A:Reference number: A30531; MUID:89035525; PMID:3263439
A:Accession: A30531
A:Molecule type: DNA
A:Residues: 1-211 <TAN>
A:Cross-references: UNIPROT:P08505; GB:M20572; NID:g341131; PIDN:AAA39302.1; PID:g387386
R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.; Sim
Eur. J. Immunol. 18, 193-197, 1988
A:Title: cDNA cloning of murine interleukin-HP1: homology with human interleukin 6.
A:Reference number: A27610; MUID:88166883; PMID:2965020
A:Accession: A27610
A:Molecule type: mRNA
A:Residues: 1-211 <VAN>
A:Cross-references: GB:X06203; NID:g52701; PIDN:CAA29560.1; PID:g52702
R:Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Cla
J. Immunol. 142, 1372-1376, 1989
A:Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
A:Reference number: A30571; MUID:89124383; PMID:2563387
A:Accession: A30571
A:Molecule type: mRNA
A:Residues: 5-211 <MOC>
A:Cross-references: GB:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699
R:Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
Eur. J. Biochem. 176, 187-197, 1988
A:Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and
A:Reference number: S01323; MUID:88329059; PMID:3262059
A:Accession: S01323

```

```

A:Molecule type: protein
A:Residues: 25-166, 'X', 168-211 <SIM>
A:Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A-
R:Grenett, H.E.; Fuentes, N.B.; Fuller, G.M.
Nucleic Acids Res. 18, 6455, 1990
A:Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
A:Reference number: S12103; MUID:91057159; PMID:2243807
A:Accession: S12103
A:Molecule type: mRNA
A:Residues: 1-211 <GRE>
A:Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728
R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
Biochem. Biophys. Res. Commun. 166, 139-145, 1990
A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
A:Reference number: A90157; MUID:90147691; PMID:2302197
A:Accession: E34047
A:Molecule type: protein
A:Residues: 66-69, 'X', 71-75; 78-94; 128-148 <JA5>
R:Van Snick, J.; Cayphas, S.; Vink, A.; Uyttenhove, C.; Coulie, P.G.; Rubira, M.R.; Simp
Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine
A:Reference number: A26662; MUID:87092311; PMID:2948184
A:Accession: A26662
A:Molecule type: protein
A:Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
A:Reference number: A40486; MUID:89017145; PMID:3262872
A:Accession: A40486
A:Molecule type: mRNA
A:Residues: 1-211 <CHI>
A:Cross-references: GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410
R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
Blood 72, 2070-2073, 1988
A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6.
A:Reference number: A60799; MUID:89062753; PMID:3264198
A:Accession: A60799
A:Molecule type: protein
A:Residues: 77-98 <SHA>
R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a mo
A:Reference number: S10241; MUID:90171860; PMID:2106569
A:Accession: S10241
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <BLA>
A:Cross-references: EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g581860
R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
Eur. J. Biochem. 217, 53-59, 1993
A:Title: Specific covalent modification of the tryptophan residues in murine interleukin-
A:Reference number: S38254; MUID:94039075; PMID:8223586
A:Accession: S38254
A>Status: preliminary
A:Molecule type: protein
A:Residues: 38-60; 75, 'X', 77-79; 176-203 <ZHA>
C:Genetics:
A:Gene: IL-6
A:Map position: 5
A:Introns: 7/1; 68/3; 106/3; 156/3
C:Superfamily: interleukin-6
C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; n
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-211/Product: interleukin-6 #status experimental <MAT>

Query Match 45.6%; Score 47; DB 1; Length 211;
Best Local Similarity 38.9%; Pred. No. 4.7;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFEF 18
Db 103 GYNQICLLKITSGLLEY 120

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C:Genetics:
A:Gene: VCAl086
A:Map position: 2
C:Superfamily: response regulator, Hnr type; response regulator homology

Query Match 44.7%; Score 46; DB 2; Length 568;
Best Local Similarity 69.2%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 SCLKKLADGFFEF 18
| | | | | | | | | |
DB 460 SSLKETPDGFFEF 472

RESULT 13
F71061
hypothetical protein PH1188 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: F71061
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, N.
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-therm
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: F71061
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-484 <KAW>
A:Cross-references: UNIPROT:O58908; GB:AP000005; NID:g3236132; PIDN:BAA30288-1;
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by
C:Genetics:
A:Gene: PH1188

Query Match 43.7%; Score 45; DB 2; Length 484;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 6; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 GENETSLCKKLADGFFEF 18
| | | | | | | | | |
DB 75 GYGKTSIMRALAGIYDY 92

RESULT 14
D70149
hypothetical protein BB0397 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: D70149
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra,
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hat
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: D70149
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-282 <KLE>
A:Cross-references: UNIPROT:O51358; GB:AE001145; NID:g2688298; PIDN:
A:Experimental source: strain B31

Query Match 42.7%; Score 44; DB 2; Length 282;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 FNETSCLKKLADGFF 16
: | | | | | | | | | |
DB 177 YNNTSGSKLEDSFF 191

```

RESULT 15
T27249
hypothetical protein Y5F2A.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27249
R:Lennard, N.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20331
A:Accession: T27249
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-454 <WIL>
A:Cross-references: UNIPROT:Q9XWL0; EMBL:AL032641; PIDN:CAR21647.1; GSPDB:GN000022; CESP:
C:Experimental source: clone Y5F2A
C:Genetics:
A:Gene: CESP:Y5F2A.4
A:Map position: 4
A:Introns: 17/2; 50/3; 125/3; 159/3; 201/3; 241/2; 353/1; 411/1
Query Match 42.7%; Score 44; DB 2; Length 454;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 10; Conservative 2; Mismatches 2; Indels 6; Gaps 1;
QY 3 NETSCLKKLA-----DGFF 16
Db 177 HETSCLKKRFVCKPCDSYF 196

Search completed: March 30, 2005, 22:06:43
Job time : 5.5157 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:12:44 ; Search time 19.9372 Seconds
(without alignments)
488.007 Million cell updates/sec

Title: US-10-828-343-2_COPY_87_105
Perfect score: 103
Sequence: 1 GFNETSCLKKLADGPFPEFE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	204	2	O40918 human herpe
2	103	100.0	204	2	O98823 human herpe
3	103	100.0	204	2	O768K3 human herpe
4	62	60.2	160	2	O97535 actus vocif
5	62	60.2	175	2	O97TH4 actus nigri
6	62	60.2	212	2	O8MKH0 salmimiri sci
7	61	59.2	209	2	O97540 actus nancy
8	61	59.2	209	2	O97TH3 actus lemur
9	61	59.2	212	1	IL6 CERTO
10	61	59.2	212	1	IL6 HUMA
11	61	59.2	212	1	IL6 MACFA
12	61	59.2	212	1	IL6 MACMU
13	58	56.3	241	2	O90Y10 gallus gall
14	55	53.4	208	1	IL6 HORSE
15	54	52.4	209	1	IL6 PHOVI
16	53	51.5	207	1	IL6 CANFA
17	53	51.5	207	2	O9MYZ7 canis famil
18	53	51.5	212	1	IL6 FIG
19	53	51.5	212	1	O8MJ75 sus scrofa
20	53	51.5	214	2	O8MKE5 sus scrofa
21	52	50.5	211	1	IL6 LAMGL
22	52	50.5	211	2	O865W7 camelus bac
23	52	50.5	892	2	O8L281 proteus vul
24	51	49.5	108	2	O9BDL5 phocoenoide
25	51	49.5	205	1	IL6 ORCOR
26	51	49.5	208	1	IL6 FELCA
27	51	49.5	208	2	O9XT80 delphinapte
28	49	47.6	207	2	O9JHH3 marmota mon
29	49	47.6	211	1	IL6 RAT
30	48.5	47.1	196	2	O92ZK2 rattus norv
31	48	46.6	162	2	O9KDW5 bacillus ha

32	48	46.6	207	1	IL6 MARMO
33	48	46.6	244	2	O6Q4I4
34	48	46.6	628	2	O96XT2
35	47	45.6	211	1	IL6 MOUSE
36	47	45.6	745	2	O8L733
37	46	44.7	186	2	O6PZ57
38	46	44.7	208	1	IL6 CAPHI
39	46	44.7	208	1	IL6 SHREP
40	46	44.7	568	2	O9KKL7
41	46	44.7	904	2	O7NAW9
42	45.5	44.2	492	1	RP54 SHEVI
43	45	43.7	148	2	O9XRE6
44	45	43.7	191	2	O7X0L4
45	45	43.7	207	2	O28403

O35736 marmota mon
O6Q4I4 lycopersico
O96XT2 sulfolobus
O8L733 mus musculus
O8L733 arabidopsis
O6PZ57 meriones un
O28319 capra hircu
P29455 ovib aries
O9KKL7 vibrio chol
O7NAW9 mycoplasma
O98012 shewanella
O9XRE6 ovib aries
O7X0L4 actinobacil
O28403 enhydra lut

ALIGNMENTS

RESULT 1
O40918 PRELIMINARY; PRT; 204 AA.
AC O40918; AC O40918; (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 26, Last annotation update)
DE OSF K2.
OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP MEDLINE=97138401; PubMed=8985427;
RX Neipel F., Albrecht J.C., Ensser A., Huang Y.Q., Li J.J.,
RA Friedman-Kien A.E., Fleckenstein B.;
RT "Human herpesvirus 8 encodes a homolog of interleukin-6.";
RL J. Virol. 71:839-842(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97296220; PubMed=9151804;
RA Neipel F., Albrecht J.C., Fleckenstein B.;
RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
human herpesvirus 8: determinants of its pathogenicity?";
RL J. Virol. 71:4187-4192(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
RA Friedman-Kien A.E., Fleckenstein B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93872; AAB62676.2; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6 MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 204 AA; 23407 MW; 2F467378200D20B9 CRC64;

Query Match 100.0%; Score 103; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFPEFE 19
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DB 87 GFNETSCLKKLADGPFPEFE 105

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RESULT 2
Q98823 ID Q98823 PRELIMINARY; PRT; 204 AA.
AC Q98823;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin-6 homolog (Fragment).
GN Name=IL-6;
OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RA Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
RA Friedman-Kien A.-B., Fleckenstein B.;
RT "Human herpesvirus 8 encodes a homologue of interleukin-6.";
RL J. Virol. 0:0-0(1996).
DR EMBL; U73655; AAB18244.1; -.
DR PDB; 1IIR; X-ray; B=..
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0008955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6 MGF GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR NON TER 204
FT SMART
SQ SEQUENCE 204 AA; 23408 MW; 1CA7772A0EDC05EB CRC64;

Query Match 100.0%; Score 103; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
DB 87 GFNETSCLKKLADGFFFE 105

RESULT 3
Q76SK3 ID Q76SK3 PRELIMINARY; PRT; 204 AA.
AC Q76SK3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ORF K2; functional interleukin-6 vIL-6 homolog (Putative interleukin 6).
OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97184526; PubMed=9032328;
RA Nicholas J., Ruvolo V., Zong J., Ciuffo D., Guo H.G., Reitz M.S.,
RA Hayward G.S.;
RT "A single 13-kilobase divergent locus in the Kaposi sarcoma-associated herpesvirus (human herpesvirus 8) genome contains nine open reading frames that are homologous to or related to cellular proteins.";
RL J. Virol. 71:1963-1974(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97208913; PubMed=9055855;
RA Nicholas J., Ruvolo V.R., Burns W.H., Sandford G., Wan X., Ciuffo D.,
RA Hendrickson S.B., Guo H.G., Hayward G.S., Reitz M.S.;
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RT "Kaposi's sarcoma-associated human herpesvirus-8 encodes homologues of macrophage inflammatory protein-1 and interleukin-6.";
RL Nat. Med. 3:287-292(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Sun R., Lin S.-F., Miller G.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBAJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094384; PubMed=8939871; DOI=10.1126/science.274.5293.1739;
RA Moore P.S., Boshoff C., Weiss R.A., Chang Y.;
RT "Molecular mimicry of human cytokine and cytokine response pathway genes by KSHV.";
RL Science 274:1739-1744(1996).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97121480; PubMed=8962146; DOI=10.1073/pnas.93.25.14862;
RA Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBAJ databases.
DR EMBL; U67774; AAB61701.1; -.
DR EMBL; U71365; AAC34937.1; -.
DR EMBL; U75698; AAC57089.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6 MGF GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 204 AA; 23408 MW; 1CA7772A0EDC05EB CRC64;

Query Match 100.0%; Score 103; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
DB 87 GFNETSCLKKLADGFFFE 105

RESULT 4
O97535 ID O97535 PRELIMINARY; PRT; 160 AA.
AC O97535;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin-6 (Fragment).
GN Name=IL-6;
OS Aotus vociferans (Spix's owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murillo L.A., Patarroyo M.E.;
RT "Identification, cloning, and sequencing of different cytokine genes in four species of owl monkey.";
RN [2]
```

RL Immunogenetics 54:645-653(2002).
 DR EMBL; AF014505; AAD01531.1; -.
 DR HSSP; P05231; IL6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 FT NON TER 1
 SQ SEQUENCE 160 AA; 17855 MW; 07A021338650A46D CRC64;

Query Match 60.2%; Score 62; DB 2; Length 160;
 Best Local Similarity 57.9%; Pred. No. 0.11;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFNETSCLKKLADGFFFE 19
 ||||:||||:|
 Db 105 GFNEETCLLKITTGLLEFE 123

RESULT 5
 Q9TH4 Q9TH4 PRELIMINARY; PRT; 175 AA.
 AC Q9TH4
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-6 (Fragment).
 GN Name=IL-6;
 OS Aotus nigriceps (Black-headed owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=57175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
 RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
 RA Murillo L.A., Patarroyo M.E.;
 RT "Identification, cloning, and sequencing of different cytokine genes
 in four species of owl monkey."
 RL Immunogenetics 54:645-653(2002).
 DR EMBL; AF097322; AAF21297.1; -.
 DR HSSP; P05231; IALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 FT NON TER 1
 SQ SEQUENCE 175 AA; 19205 MW; 2BCCE574CB99B189 CRC64;

Query Match 60.2%; Score 62; DB 2; Length 175;
 Best Local Similarity 57.9%; Pred. No. 0.12;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFNETSCLKKLADGFFFE 19
 ||||:||||:|
 Db 105 GFNEETCLLKITTGLLEFE 123

Db 105 GFNEETCLLKITTGLLEFE 123
 RESULT 6
 Q8MKH0 Q8MKH0 PRELIMINARY; PRT; 212 AA.
 ID Q8MKH0
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-6.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;
 RA Heraud J.M., Lavergne A., Kazanji M.;
 RT "Molecular cloning, characterization, and quantification of squirrel
 monkey (Saimiri sciureus) Th1 and Th2 cytokines."
 RL Immunogenetics 54:20-29(2002).
 DR EMBL; AF294757; AAK92044.1; -.
 DR HSSP; P05231; IL6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 SQ SEQUENCE 212 AA; 23581 MW; FF22CBF493245479 CRC64;

Query Match 60.2%; Score 62; DB 2; Length 212;
 Best Local Similarity 57.9%; Pred. No. 0.14;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFNETSCLKKLADGFFFE 19
 ||||:||||:|
 Db 105 GFNEETCLLKITTGLLEFE 123

RESULT 7
 Q97540 Q97540 PRELIMINARY; PRT; 209 AA.
 ID Q97540
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-6 (Fragment).
 GN Name=IL-6;
 OS Aotus nancymae (Ma's night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=37293;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
 RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
 RA Murillo L.A., Patarroyo M.E.;
 RT "Identification, cloning, and sequencing of different cytokine genes
 in four species of owl monkey."
 RL Immunogenetics 54:645-653(2002).
 DR EMBL; AF014510; AAD01536.1; -.
 DR HSSP; P05231; IALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.

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DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
FT NON_TER 209
SQ SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match 59.2%; Score 61; DB 2; Length 209;
Best Local Similarity 57.9%; Pred. No. 0.2;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 105 GFNETCLVKIITGLLEFE 123

RESULT 8
Q9TTH3 PRELIMINARY; PRT; 209 AA.
AC Q9TTH3;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Interleukin-6 (Fragment).
GN Name=IL-6;
OS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=43147;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murrillo L.A., Patarroyo M.E.,
RT "Identification, cloning, and sequencing of different cytokine genes
in four species of owl monkey."
RL Immunogenetics 54:645-653(2002).
DR EMBL; AF097323; AAF21298.1; -.
DR HSSP; P05231; 1ALU.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
FT NON_TER 209
SQ SEQUENCE 209 AA; 23115 MW; A0A3DFAA4BF560CC CRC64;

Query Match 59.2%; Score 61; DB 2; Length 209;
Best Local Similarity 57.9%; Pred. No. 0.2;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 105 GFNETCLVKIITGLLEFE 123

us-10-828-343-2_copy_87_105.rup
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RESULT 9
IL6_CERTO
ID IL6_CERTO STANDARD; PRT; 212 AA.
AC P46650;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1];
RP SEQUENCE FROM N.A.
RX STRAIN=FUJ;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation, in
hepatocytes it induces acute phase reactants.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
with the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC
CC HSSP; L26032; AAA99972.1; -.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 Interleukin-6.
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 212 AA; 23668 MW; C73C035226B4B9F CRC64;

Query Match 59.2%; Score 61; DB 1; Length 212;
Best Local Similarity 57.9%; Pred. No. 0.21;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 105 GFNETCLVKIITGLLEFE 123

RESULT 10
IL6_HUMAN
ID IL6_HUMAN STANDARD; PRT; 212 AA.
AC P05231; Q9UCU2; Q9UCU3; Q9UCU4;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
```


DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-6 precursor (IL-6) (B-cell stimulatory factor 2) (BSF-2)
DE (interferon beta-2) (Hybridoma growth factor) (CTL differentiation
DE factor) (CDF).
GN Name=IL6; Synonyms=IFNB2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=87065033; PubMed=3491322;
RA Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
RA Kashiwamura S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunasawa S.,
RA Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
RT "Complementary DNA for a novel human interleukin (BSF-2) that induces
RT B lymphocytes to produce immunoglobulin.";
RL Nature 324:73-76(1986).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=88082664; PubMed=3500852;
RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
RA Nakai S., Kishimoto T.;
RT "Structure and expression of human B cell stimulatory factor-2 (BSF-
RT 2/IL-6) gene.";
RL EMBO J. 6:2939-2945(1987).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=87067433; PubMed=3538015;
RA May L.T., Helfgott D.C., Sehgal P.B.;
RT "Anti-beta-interferon antibodies inhibit the increased expression of
RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
RT structural studies of the beta 2 interferon involved.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=87053818; PubMed=3023045;
RA Zilberstein A., Ruggieri R., Korn J.H., Revel M.;
RT "Structure and expression of cDNA and genes for human interferon-beta-
RT 2, a distinct species inducible by growth-stimulatory cytokines.";
RL EMBO J. 5:2529-2537(1986).
RN [5]
RN SEQUENCE FROM N.A.
RX MEDLINE=88089768; PubMed=3320204;
RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
RA Aarden L.A.;
RT "Molecular cloning and expression of hybridoma growth factor in
RT Escherichia coli.";
RL J. Immunol. 139:4116-4121(1987).
RN [6]
RN SEQUENCE FROM N.A.
RX MEDLINE=89391959; PubMed=2789513;
RA Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
RT "Deletion of 3' untranslated region of human BSP-2 mRNA causes
RT stabilization of the mRNA and high-level expression in mouse NIH3T3
RT cells.";
RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
RN [7]
RN SEQUENCE FROM N.A.
RX MEDLINE=87004683; PubMed=3758081;
RA Haegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
RA Fiers W.;
RT "Structural analysis of the sequence coding for an inducible 26-kDa
RT protein in human fibroblasts.";
RL Eur. J. Biochem. 159:625-632(1986).
RN [8]
RN SEQUENCE FROM N.A.
RX MEDLINE=89193117; PubMed=3266463;
RA Wong G., Witek-Giannotti J., Hewick R., Clark S., Ogawa M.;
RT "Interleukin 6: identification as a hematopoietic colony-stimulating
RT factor.";
RL Behring Inst. Mitt. 83:40-47(1988).

RN [9]
RX SEQUENCE FROM N.A.
RX MEDLINE=93178270; PubMed=1291290;
RA Chen Q.Y.;
RT "Stable and efficient expression of human interleukin-6 cDNA in
RT mammalian cells after gene transfer.";
RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
RN [10]
RN SEQUENCE FROM N.A., AND VARIANTS SER-32 AND VAL-162.
RX Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [11]
RN SEQUENCE FROM N.A.
RX TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RX SEQUENCE OF 30-63.
RX MEDLINE=88154445; PubMed=3279116;
RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
RA Billiau A.;
RT "Separation and comparison of two monokines with lymphocyte-activating
RT factor activity: IL-1 beta and hybridoma growth factor (HGF).
RT Identification of leukocyte-derived HGF as IL-6.";
RL J. Immunol. 140:1534-1541(1988).
RN [13]
RX SEQUENCE OF 30-50.
RX MEDLINE=90121567; PubMed=2610854;
RA Ming J.E., Cernetti C., Steinman R.M., Granelli-Piperno A.;
RT "Interleukin 6 is the principal cytolytic T lymphocyte differentiation
RT factor for thymocytes in human leukocyte conditioned medium.";
RL J. Mol. Cell. Immunol. 4:203-211(1989).
RN [14]
RX SEQUENCE OF 30-40, AND GLYCOSYLATION.
RX MEDLINE=91355644; PubMed=1883960; DOI=10.1016/1043-4666(91)90018-9;
RA May L.T., Shaw J.E., Khanna A.K., Zabriskie J.B., Sehgal P.B.;
RT "Marked cell-type-specific differences in glycosylation of human
RT interleukin-6.";
RL Cytokine 3:204-211(1991).
RN [15]
RX SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING FIRST DISULFIDE BOND.
RX MEDLINE=95154344; PubMed=7851440;
RA Breton J., la Fira A., Bertolero F., Orsini G., Valsasina B.,
RA Ziliotto R., de Filippis V., Polverino de Laureto P., Fontana A.;
RT "Structure, stability and biological properties of a N-terminally
RT truncated form of recombinant human interleukin-6 containing a single
RT disulfide bond.";
RL Eur. J. Biochem. 227:573-581(1995).
RN [16]
RX DISULFIDE BONDS.
RX MEDLINE=89286115; PubMed=2472117;

RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
RT "Dieulfide structures of human interleukin-6 are similar to those of
RT human granulocyte colony stimulating factor";
RL Arch. Biochem. Biophys. 272:144-151(1989).
RN [17]
RP MUTAGENESIS.
RX MEDLINE=91243808; PubMed=2037043; DOI=10.1016/0014-5793(91)80491-K;
RA Lueticken C., Kruetgen A., Moeller C., Heinrich P.C., Rose-John S.;
RT "Evidence for the importance of a positive charge and an alpha-helical
RT structure of the C-terminus for biological activity of human IL-6";
RL FEBS Lett. 282:265-267(1991).
RN [18]
RP STRUCTURE BY NMR.
RX MEDLINE=96134845; PubMed=8555185; DOI=10.1021/bi951949e;
RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
RT "Folding topologies of human interleukin-6 and its mutants as studied
RT by NMR spectroscopy";
RL Biochemistry 35:273-281(1996).
RN [19]
RP STRUCTURE BY NMR.
RX MEDLINE=97303053; PubMed=9159484; DOI=10.1006/jmbi.1997.0933;
RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
RA Cumming D.A.;
RT "Solution structure of recombinant human interleukin-6";
RL J. Mol. Biol. 268:468-481(1997).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=97224126; PubMed=9118960; DOI=10.1093/emboj/16.5.989;
RA Somers W., Stahl M., Sehara J.S.;
RT "1.9-A crystal structure of interleukin 6: implications for a novel
RT mode of receptor dimerization and signaling";
RL EMBO J. 16:989-997(1997).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -!- DATABASE: NAME=RED Systems' cytokine mini-reviews; IL6;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=208".

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Query Match 59.2%; Score 61; DB 1; Length 212;
Best Local Similarity 57.9%; Pred. No. 0.21;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKLADGFFPE 19
DB 105 GFNETCLVKIITGLLEFE 123

RESULT 11

IL6_MACFA STANDARD; PRT; 212 AA.
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.

OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tateumi M.;
RT "Molecular cloning and expression of cynomolgus monkey interleukin-
RT 6";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.

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DR HSSP; AB000554; BAA19148.1; -;
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 Interleukin-6.
FT DISULFD 72 78 By similarity.
FT DISULFD 101 111 By similarity.
FT CARBOHYD 73 73 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 172 172 N-linked (GLCNAC. .) (Potential).
SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBF0B0389 CRC64;

Query Match 59.2%; Score 61; DB 1; Length 212;
Best Local Similarity 57.9%; Pred. No. 0.21;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKLADGFFPE 19
DB 105 GFNETCLVKIITGLLEFE 123

RESULT 12

IL6_MACMU STANDARD; PRT; 212 AA.
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAC 2;
RX MEDLINE=96003435; PubMed=7561102;
RA Villingier F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";

RL J. Immunol. 155:3946-3954 (1995).
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC
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 CC
 DR EMBL; L26028; RAA99978.1; --
 DR HSP; P05231; IALU.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 By similarity.
 FT CHAIN 30 212 Interleukin-6.
 FT DISULFID 72 78 By similarity.
 FT DISULFID 101 111 By similarity.
 FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
 FT SEQUENCE 212 AA; 23728 MW; 4130DF0CF0BCCAD CRC64;
 Query Match 59.2%; Score 61; DB 1; Length 212;
 Best Local Similarity 57.9%; Pred. No. 0.21;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLKLAGDFFFE 19
 DB 105 GFNETCLVXIITGLLEFE 123
 RESULT 13
 Q90Y10 PRELIMINARY; PRT; 241 AA.
 AC Q90Y10;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Interleukin-6 precursor.
 GN Names=IL-6;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schneider K., Klaas R., Kaspers B., Staeheli P.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J.,
 RA Wigley P.;
 RT "Differential cytokine expression in avian cells in response to
 RT invasion by Salmonella typhimurium, Salmonella enteritidis and
 RT Salmonella gallinarum."; Microbiology 146:3217-3226 (2000).
 RN [3]

RP SEQUENCE FROM N.A.
 RA Kaiser P.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ309540; CAC40812.1; --
 DR EMBL; AJ250838; CAC15566.2; --
 DR HSP; P05231; IALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD008388; GCSF_MGF; 1.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Signal.
 FT SIGNAL 1 47 Potential.
 FT CHAIN 48 241 mature ChIL-6.
 SQ SEQUENCE 241 AA; 26790 MW; 657F8049F25BD2F8 CRC64;
 Query Match 56.3%; Score 58; DB 2; Length 241;
 Best Local Similarity 52.8%; Pred. No. 0.7;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLKLAGDFFFE 19
 DB 126 GFDEKCLTKLSGLFAFQ 144
 RESULT 14
 IL6 HORSE
 ID IL6 HORSE STANDARD; PRT; 208 AA.
 AC Q95181; O19007; O46568;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Names=IL6;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20579380; PubMed-11137120; DOI=10.1016/S0165-2427(00)00241-5;
 RA Swiderski C.E., Sobol G., Lunn D.P., Horobov D.W.;
 RT "Molecular cloning, sequencing, and expression of equine interleukin-
 RT 6."; Vet. Immunol. Immunopathol. 77:213-220 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
 RT "Molecular cloning of equine interleukin-6."; Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lai A.C.K.;
 RT "Cloning and expression of equine interleukin-6."; Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC
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DR EMBL; U64794; AAB87703.1; -.
DR EMBL; AF005227; AAB62246.1; -.
DR EMBL; AF041975; AAC04574.1; -.
DR PIR; T09216; T09216.
DR HSSP; P05231; 1IL6.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 208 Interleukin-6.
FT DISULFID 69 75 By similarity.
FT DISULFID 98 108 By similarity.
FT CARBOHYD 71 71 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CONFLICT 4 5 LS -> FF (in Ref. 1).
FT CONFLICT 8 8 T -> A (in Ref. 3).
FT CONFLICT 137 137 I -> V (in Ref. 2).
FT CONFLICT 205 205 V -> I (in Ref. 3).
SQ SEQUENCE 208 AA; 23325 MW; A62F4C234056BF66 CRC64;

Query Match 53.4%; Score 55; DB 1; Length 208;
Best Local Similarity 47.4%; Pred.No. 1.8;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 GFNETSCLKKLADGPFPE 19
DB 102 GFNETCLMKITGLSEFQ 120

RESULT 15
IL6 PHOVI
ID IL6_PHOVI STANDARD; PRT; 209 AA.
AC Q28519.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6) (Fragment).
GN Name=IL6;
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
OX NCBI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817; DOI=10.1007/s002510050045;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hammi K.D.,
RA Stott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.

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DR EMBL; L46802; AAB01430.1; -.
DR HSSP; P05231; 1IL6.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT NON_TER 1 1
FT SIGNAL <1 26 By similarity.
FT CHAIN 27 209 Interleukin-6.
FT DISULFID 69 75 By similarity.
FT DISULFID 98 108 By similarity.
SQ SEQUENCE 209 AA; 23483 MW; 75144922B43B48E9 CRC64;

Query Match 52.4%; Score 54; DB 1; Length 209;
Best Local Similarity 42.1%; Pred.No. 2.6;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 GFNETSCLKKLADGPFPE 19
DB 102 GFNETCLTRITTLGLRFQ 120

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Job time : 20.9372 secs